

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw mode1

Run on: July 20, 2005, 17:41:40 ; Search time 442 Seconds

(without alignments)

294.648 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugacucacucugaggcuctt 22

Scoring table: OLIGO_NUC Gapox_60.0 , Gapext 60.0

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Post-processing: Listing first 300 summaries

Database : N_GenSeq_16Dec04:*

1: -_genSeqn1980s:*

2: _genSeqn1990s:*

3: _genSeqn2000s:*

4: _genSeqn2001s:*

5: _genSeqn20010s:*

6: _genSeqn2002as:*

7: _genSeqn2002bs:*

8: _genSeqn2003as:*

9: _genSeqn2003bs:*

10: _genSeqn2003cs:*

11: _genSeqn2003ds:*

12: _genSeqn2004as:*

13: _genSeqn2004bs:*

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	90.9	29751	12	ADJ39000		Adj39000 SARS CORO
2	16	72.7	619	10	ADKS5384		AdKS5384 Plant DNA
3	16	72.7	619	10	ADKS57664		AdKS57664 Plant DNA
4	16	72.7	619	11	ADM45449		AdM45449 Insect re
5	16	72.7	672	10	ADM44886		AdM44886 Insect re
6	16	72.7	686	10	ADKS57646		AdKS57646 Plant DNA
7	16	72.7	686	10	ADKS5332		AdKS5332 Plant DNA
8	16	696	11	ADM45452		AdM45452 Insect re	
9	15	68.2	534	6	ABN69216		Abn69216 Streptococ
10	15	68.2	537	8	ACAS0576		Acas0576 Prokaryot
c 11	15	68.2	627	6	ABS61473		AbS61473 Prokaryot
c 12	15	68.2	1101	13	ADR61500		AdR61500 Cotton cD
c 13	15	68.2	1191	5	ABA14473		AbA14473 Human ner
c 14	15	68.2	1191	4	ABA14472		AbA14472 Human ner
c 15	15	68.2	1820	4	AAI22168		Aai22168 Probe #12
c 16	15	68.2	1820	4	ABA67247		AbA67247 Human fo
c 17	15	68.2	1820	4	ABA47467		Aba47467 Probe #16
c 18	15	68.2	1820	4	ABA9335		AbA9335 Human bre
c 19	15	68.2	1820	4	ABA34342		Aba34342 Probe #12
c 20	15	68.2	1820	4	AAK15686		Aak15686 Human bra
							Aai07869 Probe #78
							AbS15429 Human gen
							AaI24124 Probe #14
							Aba9247 Human fo
							AaI49420 Probe #15
							AbA51239 Human bre
							Aba16163 Probe #14
							Aak43349 Human bon
							Aak17541 Human bra
							Aab17430 Human gen
							Aai12930 Probe #28
							AbA54631 Human fo
							Aai34291 Probe #29
							AbA44181 Human bre
							Aba24415 Probe #28
							AbA2920 Human bra
							AaI02849 Probe #28
							AbS02874 Human gen
							AbD37626 Human nuc
							AbD01842 Drosophil
							AbD10358 Drosophil
							AbD104554 Drosophil
							AbD14707 Human NF-
							AbD442 Arabidops
							Aac53227 Arabidops
							Adr45310 Bacterial
							Aaf45310 Bacterial
							Aaf19998 Human CDN
							Abn92664 Staphyloc
							AbD01314 Staphyloc
							Abn9215 Streptoco
							Abn65215 Streptoco
							AbC3227 Arabidops
							AcT70959 Photorhab
							AcT8159 Rice cent
							AdE16656 B. hensel
							AdE55033 Rat gene
							AdE55037 Rat gene
							AcT70959 Photorhab
							Aah5485 S. epider
							AdB69029 C. neofor
							Aca6688 Prokaryot
							Aas79450 DNA encod
							Aas79450 DNA encod
							Aah5329 S. epider
							AbD102454 Drosophil
							AbD16655 B. hensel
							AbD28159 Mouse Wnt
							AbD72287 Mouse Wnt
							AbD95797 Mouse Wnt
							AbD33385 Human c-r
							AbD184182 Human c-r
							Continuation (8 of 8)
							Abn71527 Streptoco
							Continuation (41 of 41)
							Continuation (8 of 8)
							AbD13752 Ostearco
							AdD59419 Human can
							AbD4625 MOL3 reve
							AbD18788 G-coupled
							Adr38524 Novel_hum
							AaQ76533 Human gen
							AbC89259 Human gen
							AbC94421 Klebsiell
							AbD12386 DNA Seq I
							Abv88798 Human col
							Abn19496 Human ORF
							Adp15241 Cotton ex
							Aaa82241 N. mening
							Abv97902 Human pan
							Abv79752 Human pan
							AbA57952 Human fo
							AbI37549 Probe #62
							Aak31673 Human bon
							Aak06027 Human bra
							AbS13357 Human liv
							AbS031357 Human gen
							AbS06429 Human adu
							ACH20490 Human adu

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	90.9	29751	12	ADJ39000		Adj39000 SARS CORO
2	16	72.7	619	10	ADKS5384		AdKS5384 Plant DNA
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6	16	72.7	686	10	ADKS57646		AdKS57646 Plant DNA
7	16	72.7	686	10	ADKS5332		AdKS5332 Plant DNA
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9	15	68.2	534	6	ABN69216		Abn69216 Streptococ
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c 13	15	68.2	1191	5	ABA14473		AbA14473 Human ner
c 14	15	68.2	1191	4	ABA14472		AbA14472 Human ner
c 15	15	68.2	1820	4	AAI22168		Aai22168 Probe #12
c 16	15	68.2	1820	4	ABA67247		AbA67247 Human fo
c 17	15	68.2	1820	4	ABA47467		Aba47467 Probe #16
c 18	15	68.2	1820	4	ABA9335		AbA9335 Human bre
c 19	15	68.2	1820	4	ABA34342		Aba34342 Probe #12
c 20	15	68.2	1820	4	AAK15686		Aak15686 Human bra

c 94	13	59.1	539	4	AAK91848	Human	CDN	Aav90767	Nucleotid	
c 95	13	59.1	539	12	ADL28275	AAK9253	Human	CDN	ABT20603	
c 96	13	59.1	539	12	ADL29680	5'	end of	ABT206	03	
c 97	13	59.1	539	12	ADL28275	Ad128275	5'	Adr18787	Aspergill	
c 98	13	59.1	539	12	ACH75524	Ach75524	Human	gen	Adr03843	
c 99	13	59.1	584	3	AAC35392	Aac35392	Arabidops	Adr13067	Arabidops	
c 100	13	59.1	585	6	ABZ13833	Abz13833	Arabidops	Adr68438	Arabidops	
c 101	13	59.1	603	10	ADK6004	Adk6004	Plant	Aav90893	Nucleotid	
c 102	13	59.1	625	6	ABV96002	Abv96002	Human	Aak94748	Human	
c 103	13	59.1	646	6	ABV99049	Abv99049	Human	pan	Adr13185	Full
c 104	13	59.1	678	4	AAS5311	Aas5311	Haemophil	Adq23265	Full	
c 105	13	59.1	816	2	AAX30429	Aax30429	H.	Pylori	Adr07315	Full
c 111	13	59.1	816	8	ACA34154	Aca34154	Prokaryot	Adr07609	Human	
c 112	13	59.1	816	4	AAS53726	Aas53726	Heicobac	Aat97609	EIA	
c 106	13	59.1	709	10	ADK56318	Adk56318	Plant	Adr84890	Aspergill	
c 107	13	59.1	714	6	ACD2613	Adc2613	Human	col	Aca2424	
c 108	13	59.1	796	6	ABN98064	Abn98064	Arabidops	Adr85477	Aspergill	
c 109	13	59.1	797	3	AAA8471	Aaa8471	Plant	Adr89905	Human	
c 110	13	59.1	840	2	AAX30465	Aax30465	H.	Pylori	Adr43659	CDNA
c 117	13	59.1	816	2	AAX30429	Aax30429	H.	Pylori	Adi50406	CDNA
c 118	13	59.1	885	3	AAC77620	Aac77620	Human	can	Adr97610	Human
c 119	13	59.1	916	6	AAC53726	Aac53726	Heicobac	Adr84890	EIA	
c 113	13	59.1	816	4	AAC53890	Aac53890	Heicobac	Abz35234	Human	
c 114	13	59.1	816	8	ACA34980	Aca34980	Heicobac	Adr20024	Aspergill	
c 115	13	59.1	833	10	ACCC3927	Accc3927	Nucleotid	Adr79063	Human	
c 116	13	59.1	840	2	AAT68162	Aat68162	H.	Pylori	Adr13871	Human
c 117	13	59.1	816	2	ABV30274	Abv30274	Human	pro	Adm24422	Human
c 118	13	59.1	885	3	AAC77620	Aac77620	Human	can	Aat97610	Tumour
c 121	13	59.1	944	6	ADK65152	Adk65152	Arabidops	Abz78236	A.	
c 120	13	59.1	947	10	ADC16634	Adc16634	Thalecres	Adr05424	Haemophil	
c 121	13	59.1	947	10	ADD30295	Ad30295	Plant	Adr05424	Human	
c 122	13	59.1	947	12	AD141550	Ad141550	Plant	Adr05424	CDNA	
c 123	13	59.1	947	12	AD001654	Ad001654	Thalecres	Adr05424	Genetic	
c 124	13	59.1	954	5	AAH65497	Aah65497	Prokaryot	Adr05424	Genetic	
c 125	13	59.1	1024	6	ADK65613	Adk65613	Heicobac	Adr05424	Genetic	
c 126	13	59.1	1024	4	AAI81237	Aai81237	Human	pol	Adr05424	Genetic
c 127	13	59.1	1065	5	AAS70168	Aas70168	DNA	Adr05424	Genetic	
c 128	13	59.1	1137	13	ADS49156	Ad49156	Bacterial	Adr05424	Genetic	
c 129	13	59.1	1140	3	AAC5746	Aac5746	Human	sec	Adr05424	Genetic
c 130	13	59.1	1146	8	ACA44595	Aca44595	Prokaryot	Adr05424	Genetic	
c 131	13	59.1	1161	10	ADR03576	Adr03576	Bacterial	Adr05424	Genetic	
c 132	13	59.1	1387	10	ADD30625	Ad30625	Plant	Adr05424	Genetic	
c 133	13	59.1	1387	12	ADT41852	Adt41852	Plant	Adr05424	Genetic	
c 134	13	59.1	1387	12	ADG62988	Adg62988	Transcrip	Adr05424	Genetic	
c 135	13	59.1	1411	6	ABN97326	Abn97326	Gene	Adr05424	Genetic	
c 136	13	59.1	1411	13	ADB86272	Adb86272	Human	hum	Adr05424	Genetic
c 137	13	59.1	1411	13	ADQ97432	Adq97432	Human	hum	Adr05424	Genetic
c 138	13	59.1	1411	13	ADQ95933	Adq95933	T	cell	Adr05424	Genetic
c 139	13	59.1	1422	12	ADQ59911	Adq59911	T	cell	Adr05424	Genetic
c 140	13	59.1	1422	12	ADQ59911	Adq59911	Human	pol	Adr05424	Genetic
c 141	13	59.1	1476	4	AAI63351	Aai63351	Human	pol	Adr05424	Genetic
c 142	13	59.1	1539	10	ADC21639	Adc21639	Thogoto	Adr05424	Genetic	
c 143	13	59.1	1546	4	AAI58565	Aai58565	Human	pol	Adr05424	Genetic
c 144	13	59.1	1546	9	ADQ98782	Adq98782	DNA	Adr05424	Genetic	
c 145	13	59.1	1583	3	AAC40650	Aac40650	Novel	Adr05424	Genetic	
c 151	13	59.1	1583	4	AAI63946	Aai63946	Human	pol	Adr05424	Genetic
c 146	13	59.1	1583	8	AAS31613	Aas31613	cDNA	Adr05424	Genetic	
c 147	13	59.1	1583	4	ABK43947	Abk43947	DNA	Adr05424	Genetic	
c 148	13	59.1	1583	12	ADT21218	Adt21218	cDNA	Adr05424	Genetic	
c 149	13	59.1	1583	12	ADT42510	Adt42510	Plant	Adr05424	Genetic	
c 150	13	59.1	1583	12	ADDB5775	Adb5775	Primary	Adr05424	Genetic	
c 157	13	59.1	1639	8	ADA73069	Ad73069	Rat	Adr05424	Genetic	
c 158	13	59.1	1791	8	ABT19398	Abt19398	Orf12	Adr05424	Genetic	
c 159	13	59.1	1791	10	ADEB1196	Adeb1196	Orf12	Adr05424	Genetic	
c 160	13	59.1	1793	12	ADT42509	Adt42509	Plant	Adr05424	Genetic	
c 154	13	59.1	1767	8	ABT121218	Abt121218	tra	Adr05424	Genetic	
c 155	13	59.1	1775	12	ADT42510	Adt42510	Primary	Adr05424	Genetic	
c 162	13	59.1	1778	10	ADDB5775	Adb5775	Primary	Adr05424	Genetic	
c 163	13	59.1	2025	8	ABT13381	Abt13381	Rat	Adr05424	Genetic	
c 164	13	59.1	2025	8	ABT21201	Abt21201	Aspergill	Adr05424	Genetic	
c 165	13	59.1	2047	6	ABL93809	Abl93809	Human	sec	Adr05424	Genetic
c 166	13	59.1	2047	8	ABX62972	Abx62972	Human	act	Adr05424	Genetic

240	13	59.1	17238	13	ADR03880	Carotenoi	XX	SARS coronavirus nucleotide sequence.
241	13	59.1	17238	13	ADR03961	Genetical	DE	
242	13	59.1	17238	13	ADR03960	Genetical	XX	
243	13	59.1	17593	13	ADR03884	Carotenoi	KW	small interfering RNA; siRNA; modified ribonucleotide sequence; hepatitis C virus; HCV; hepatitis C; viral replication inhibition; hepatitis C virus; hepatitis C virus; hepatitis C virus; hepatitis C virus; antiinflammatory; hepatotropic; virucide; hepatitis A virus; hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus; rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus; metapneumovirus; coronavirus; viral infection; gene; ds.
244	13	59.1	17593	13	ADR03964	Genetical	KW	
245	13	59.1	17595	13	ADR03889	Carotenoi	KW	
246	13	59.1	17756	13	ADR03969	Genetical	KW	
247	13	59.1	17756	13	ADR03879	Carotenoi	KW	
248	13	59.1	17877	13	ADR03879	Genetical	KW	
249	13	59.1	18333	13	ADR03893	Carotenoi	KW	
250	13	59.1	18333	13	ADR03973	Genetical	OS	
251	13	59.1	18449	13	ADR03882	Carotenoi	XX	
252	13	59.1	18449	13	ADR03891	Carotenoi	PN	WO2004011647-A1.
253	13	59.1	18449	13	ADR03883	Carotenoi	XX	
254	13	59.1	18449	13	ADR03962	Genetical	PD	05-FEB-2004.
255	13	59.1	18449	13	ADR03963	Genetical	XX	
256	13	59.1	18449	13	ADR03973	Genetical	PF	25-JUL-2003; 2003WO-US023104.
257	13	59.1	18617	13	ADR03892	Carotenoi	XX	
258	13	59.1	18617	13	ADR03972	Genetical	PR	26-JUL-2002; 2002US-0398605P.
259	13	59.1	19491	13	ADR03887	Carotenoi	XX	
260	13	59.1	19491	13	ADR03967	Genetical	PA	(CHIR) CHIRON CORP.
261	13	59.1	21300	13	ADR03888	Carotenoi	XX	
262	13	59.1	21300	13	ADR03968	Genetical	PI	Han J, Seo MY, Houghton M;
263	13	59.1	23118	4	AAK71708	Human imm	XX	
264	13	59.1	23171	11	ACN44326	Human gen	DR	WPI; 2004-143862/14.
265	13	59.1	23751	12	ADQ9500	Human can	XX	
C 266	13	59.1	29598	2	AAV49554	Human SC2	PT	New RNase resistant small interfering RNA, useful for treating viral infections, e.g., hepatitis C, influenza virus or coronavirus infection.
C 267	13	59.1	32349	4	ABL1530	Drosophil	XX	
C 268	13	59.1	52312	13	ABD3555	Murine ca	XX	Example 10; Fig 3; 74pp; English.
C 269	13	59.1	59767	13	ABD32905	Murine can	PS	New RNase resistant small interfering RNA (siRNA) which comprises a modified ribonucleotide, where the siRNA is resistant to
C 270	13	59.1	68750	3	Aaz25887	Sorangium	XX	comprises a modified ribonucleotide, where the siRNA is resistant to
C 271	13	59.1	72149	10	ADDB95173	ML-336B 8	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 272	13	59.1	85814	13	ADT05644	Haemophil	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 273	13	59.1	91823	10	ADL13497	Osteoarthr	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 274	13	59.1	94618	3	AAF22285	BAC conta	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 275	13	59.1	96593	9	ADA0260	Human RUN	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 276	13	59.1	96593	10	ADB73338	Human RUN	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 277	13	59.1	96593	10	AdB95848	Human RUN	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 278	13	59.1	96593	9	ADA02981	Mouse Map	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 279	13	59.1	96599	10	ADB7219	Cancer Map	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 280	13	59.1	96599	10	ADCB8461	Mouse Map	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 281	13	59.1	96599	12	ADM74576	Mouse ca	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 282	13	59.1	110000	2	AAT42063	Continuation (6 of	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 283	13	59.1	110000	11	ACN44998	Ab188122	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 284	13	59.1	174424	6	ABL68122	_	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 285	13	59.1	177380	8	ACF622751	Act67751	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 286	13	59.1	177380	10	ADB20870	Mouse can	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 287	13	59.1	177380	10	ADB87959	Human UGT	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 288	13	59.1	177380	10	ADB96342	Human MDR	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 289	13	59.1	177380	10	ADB21333	Human MDR	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 290	13	59.1	181343	12	ADQ19573	Human sof	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 291	13	59.1	198468	12	ADQ97831	Mouse can	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 292	13	59.1	203654	10	ABX16034	Human gen	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 293	13	59.1	209484	11	ACN44126	Human gen	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 294	13	59.1	220224	11	ACN44702	Human gen	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 295	13	59.1	220803	13	ABD32730	Abc322730	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 296	13	59.1	234980	5	AAH68525	C Glutami	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 297	12	54.5	25	9	ACK27997	Human mic	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 298	12	54.5	25	9	ACI79106	Human mic	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 299	12	54.5	25	9	ACI12036	Human mic	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
C 300	12	54.5	27	2	AAX80816	A.thalian	CC	comprises a modified ribonucleotide, where the siRNA is resistant to
ALIGNMENTS								
RESULT 1								
ADJ39000	XX							
ID ADJ39000	AC							
XX								
06-MAY-2004	(first entry)							

Query Match 1 GUGACUCACUCGAGAGCUC 20
Best Local Similarity 90.9%; Score 20; DB 12; Length 29751;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;Query Match 2 ADKS8384 20
Best Local Similarity 75.0%; Score 75; DB 10; Length 29751;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
DB 776 GTGAACTACTGAGTC 795RESULT 2 ADKS8384
ID ADKS8384 standard; DNA; 619 BP.
XX

AC ADK58384; XX
 DT 06-MAY-2004 (first entry)
 DE Plant DNA sequence which confers altered metabolic characteristic #5767.
 PT altered metabolic characteristic; plant; acid metabolism;
 alcohol metabolism; fatty acid metabolism;
 branched fatty acid metabolism; alkaid metabolism;
 amino acid metabolism; ester metabolism; glyceride metabolism;
 phenolic metabolism; carbohydrate metabolism; sterol metabolism;
 terpene metabolism; isoprenoid metabolism; alkanes metabolism;
 alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
 quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
 XX Unidentified.
 OS XX
 PN WO2003020936-A1.
 PD 13-MAR-2003.
 PF 30-AUG-2002; 2002WO-US027884.
 XX PR 31-AUG-2001; 2001US-0316471P.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 PA (DOWC) DOW CHEM CO.
 PA (DOWC) DOW AGROSCIENCES LLC.
 PT Novel genes that confer altered metabolic characteristics in Nicotiana
 PT benthamiana plants, useful for altering the levels of metabolites e.g.
 PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
 DR WPI; 2003-313091/30.
 PS SEQ ID NO 5047; 2576pp; English.
 XX The invention comprises DNA sequences which confer an altered metabolic
 CC characteristic when they are expressed in a plant. The DNA sequences of
 CC the invention are useful for producing plants with an altered metabolic
 CC characteristic, such as: altered acid metabolism, alcohol metabolism, or other
 CC fatty acid metabolism, branched fatty acid metabolism, alkaloid or other
 CC base metabolism, altered amino acid metabolism, altered ester metabolism,
 CC altered glyceride metabolism, altered phenolic metabolism, altered
 CC carbohydrate metabolism, altered sterol, oxygenated terpene, or
 CC isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
 CC metabolism, ketone or quinone metabolism. The DNA sequences of the
 CC invention may be used to provide disease resistance in a plant and gene
 CC shuffling or sexual PCR procedures. The present nucleic acid represents a
 CC DNA sequence of the invention.
 XX Sequence 619 BP; 133 A; 183 C; 177 G; 126 T; 0 U; 0 Other;
 SQ Query Match 72.7%; Score 16; DB 10; Length 619;
 Best Local Similarity 75.0%; Pred. No. 7.4;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 CUCACUGGAGGCT 21.
 DB 599 CTCACCTCGTGAGCTCT 614
 RESULT 4
 ID ADM45449 standard; DNA; 619 BP.
 XX AC ADM45449;
 XX DT 03-JUN-2004 (first entry)
 DE Insect resistance associated DNA sequence SeqID856.
 XX KW insect resistant phenotype; plant; protectant; gene therapy;
 XX KW Arabidopsis thaliana; Nicotiana benthamiana; Oryza sativa;
 XX KW Papaver rhoeas; rice; insect resistance; insect-resistant plant; ds.
 AC ADK57664;
 XX DT 06-MAY-2004 (first entry)
 DE Plant DNA sequence which confers altered metabolic characteristic #5047.

OS Unidentified.

XX PT New isolated nucleic acid having expression that results in an insect
PN PT resistant phenotype, useful for conferring insect resistance and for
XX PT producing insect-resistant plants.

XX PD 13-MAR-2003.

XX PF 30-AUG-2002; 2002WO-US027882.

XX PR 31-AUG-2001; 2001US-0316319P.

XX (DOWC) DOW CHEM CO.

XX PA Shukla V, Meade T, Larrinua I;

XX DR WPI; 2003-290133/28.

XX New isolated nucleic acid having expression that results in an insect
PT resistant phenotype, useful for conferring insect resistance and for
PT producing insect-resistant plants.

XX Claim 1; SEQ ID NO 856; 396pp; English.

XX This invention relates to a novel isolated nucleic acid comprising, or
CC hybridising under low stringent conditions to, any of the 1214 nucleic
CC acid sequences given in the specification, where the expression of the
CC nucleic acid in a plant results in an insect resistant phenotype. The
CC invention may be useful as a plant protectant or for gene therapy. The
CC genes are derived from *Arabidopsis thaliana*, *Nicotiana benthamiana*, *Oryza*
CC *sativa* and *Papaver rhoes*. The isolated nucleic acid and vector are
CC useful for conferring insect resistance and for producing insect-
CC resistant plants. The present sequence is that of a DNA sequence of the
CC invention which may confer insect resistance to plants.

XX Sequence 619 BP; 133 A; 177 C; 126 G; 126 T; 0 U; 0 Other;

XX Query Match 72.7%; Score 16; DB 11; Length 619;

XX Best Local Similarity 75.0%; Pred. No. 7.4;

XX Matches 12; Conservative 4; Nismatches 0; Indels 0; Gaps 0;

XX Plant DNA sequence which confers altered metabolic characteristic #5029.

XX RESULT 6

XX ADD57646 ADD57646 standard; DNA; 686 BP.

XX AC ADD57646;

XX DT 06-MAY-2004 (first entry)

XX XX

XX Plant DNA sequence which confers altered metabolic characteristic #5029.

XX KW altered metabolic characteristic; plant; acid metabolism;

XX KW alcohol metabolism; fatty acid metabolism;

XX KW branched fatty acid metabolism; alkaloid metabolism;

XX KW amino acid metabolism; ester metabolism; glyceride metabolism;

XX KW phenolic metabolism; carbohydrate metabolism; sterol metabolism;

XX KW terpene metabolism; isoprenoid metabolism; alkene metabolism;

XX KW alkyne metabolism; hydrocarbon metabolism; ketone metabolism;

XX KW quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds .

XX Unidentified.

XX OS WO2003020936-A1.

XX XX

XX PD 13-MAR-2003.

XX PN 30-AUG-2002; 2002WO-US027884.

XX PR 31-AUG-2001; 2001US-0316471P.

XX XX

XX (DOWC) DOW CHEM CO.

XX PA (DOWC) DOW AGROSCIENCES LLC.

XX PN Weglarz T, Gachotte D, Blakeslee B, McCREARY DA, Pell RJ,
XX PI Miller BA;

XX PD Oriello JV, Croley R, Reddy AS, Shukla V, Larrinua I, Miller BA;

XX DR WPI; 2003-313091/30.

XX New genes that confer altered metabolic characteristics in *Nicotiana*
PT *benthamiana* plants, useful for altering the levels of metabolites e.g.
PT acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.

XX Claim 1; SEQ ID NO 5029; 2576pp; English.

XX The invention comprises DNA sequences which confer an altered metabolic

XX CC

Db 622 CTCACCTGAGCTCT 637

RESULT 9

ABN6216 ID ABN6216 standard; DNA; 534 BP.

XX DT 01-JUN-2002 (first entry)

DE Streptococcus polynucleotide SBQ ID NO 6345.

XX Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; Group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.

XX Streptococcus pyogenes.

OS PN WO200234771-A2.

XX PD 02-MAY-2002.

XX PP 29-OCT-2001; 2001WO-GB004789.

XX PR 27-OCT-2000; 2000GB-00026333.

PR 24-NOV-2000; 2000GB-00028727.

PR 07-MAR-2001; 2001GB-00005640.

XX (CHIR-) CHIRON SPA.

PA (GENO-) INST GENOMIC RES.

PI Tettelin H, Massignani V, Margarit Y Rossi, Grandi G, Fraser C;

PI Tettelin H, 2002-352536/38.

XX DR P-PSDB; ABP28585.

PS New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.

PT Claim 7; Page 3799; 4525pp; English.

PT New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

PT detecting a compound that binds to the protein.

XX CC The invention relates to a protein (ABP05413-ABP0895) from group B streptococcus (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (1) nucleic acids encoding (1), ABN65044-ABN71526 and antibodies that bind (1) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.

CC Nucleic acids encoding (1) are used to detect Streptococcus in a biological sample. (1) is used to determine whether a compound binds to (1). A composition comprising (1) or a nucleic acid encoding (1), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (1) may be used to recombinantly produce (1) and may be used in gene therapy. Antibodies to (1) are used for affinity chromatography, immunoassays, and distinguishing/identifying Streptococcus proteins.

XX SQ Sequence 534 BP; 186 A; 101 C; 109 G; 138 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 6; Length 534;

Best Local Similarity 80.0%; Pred. No. 29;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAACUCUCCUGAG 17

Db 94 GAACTCACTCGTGAG 108

RESULT 10

AC50276 standard; DNA; 537 BP.

XX ID AC50276

XX AC AC50276;

XX DT 19-JUN-2003 (first entry)

DE Prokaryotic essential gene #31933.

XX KW Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

XX KW Strptococcus pyogenes.

OS PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PP 21-MAR-2002; 2002WO-US009107.

XX PD 02-MAY-2002.

XX PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0361699P.

XX PA (ELITR-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029326/02.

XX DR P-PSDB; ABU46106.

XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

XX PS Claim 14; SEQ ID NO 38146; 1766pp; English.

CC The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid encoding the polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against biological pathway (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX Sequence 537 BP; 188 A; 101 C; 109 G; 139 T; 0 U; 0 Other;
 SQ Query Match 68.2%; Score 15; DB 8; Length 537;
 Best Local Similarity 80.0%; Pred. No 29;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 GAAUCACUGUGAG 17
 Db 94 GRACTCACTCGTGAG 108

RESULT 11
 ABS1473 C
 ABS1473 standard; cDNA; 627 BP.
 XX DT 05-NOV-2002 (first entry)
 DE Prostate specific nucleic acid DEX0259_81.
 XX Human; ss; prostate specific nucleic acid; PSNA; prostate cancer;
 KW cytosolic; non-cancerous prostate disease; PSP; vaccine;
 KW prostate specific protein; metastasis
 XX OS Homo sapiens.
 XX PN WO2002422776-A2.
 XX PD 30-MAY-2002.
 XX PR 01-NOV-2001; 2001WO-US045654.
 XX PR 01-NOV-2000; 2000US-0244782P.
 XX PA (DIAD-) DIADEXUS INC.
 PI Sun Y, Recipon H, Chen S, Liu C;
 XX DR 2002-490217/52.
 XX PT New polypeptide useful for diagnosing and monitoring the presence and
 PT databases of prostate cancer in a patient and as a component in
 PT search analysis as well as in sequence analysis algorithms.
 XX PS Claim 1; Page 183-184; 242pp; English.
 XX The invention relates to an isolated polypeptide comprising a sequence
 CC with 60 % identity to one of prostate specific protein (PSP) sequences,
 CC or comprising an amino acid sequence encoded by one of 136 nucleotide
 CC prostate specific nucleic acids sequences, PSNA, (or a sequence that
 CC hybridises to it or is 60% identical to it), given in the specification.
 CC Also included are a vector comprising the polynucleotide, a host cell
 CC comprising the vector an antibody specific for the PSP proteins and a
 CC vaccine comprising the protein or polynucleotide. The PSP and PSNA are
 CC useful for diagnosing and monitoring the presence and metastases of
 CC prostate cancer in a patient. The PSNA is useful for determining the
 CC level PSNA in a sample. An antibody to the PSP is useful for determining
 CC the presence of prostate specific protein in a sample, and for treating a
 CC patient with prostate cancer, which induces an immune response against
 CC the prostate cancer cell expressing the nucleic acid or polypeptide and a
 CC kit useful for detecting a risk of cancer or presence of cancer in a
 CC patient. PSNA is useful as hybridisation probes to detect, characterise
 CC and quantify hybridising nucleic acids from both genomic and transcript-
 CC derived nucleic acid samples and also in microarrays. Sequences of PSP
 CC and PSNA are useful as components in databases for search analysis as
 CC well as in sequence analysis algorithms. PSNA is useful to drive in vivo
 CC expression of PSP. The present sequence is a PSNA of the invention
 XX Sequence 627 BP; 129 A; 152 C; 169 G; 177 T; 0 U; 0 Other;
 SQ Query Match 68.2%; Score 15; DB 6; Length 627,

Best Local Similarity 80.0%; Pred. No 29;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 GAAUCACUGUGAG 17
 Db 224 GAACTCACTCGTGAG 210

RESULT 12
 ADR61500 standard; cDNA; 1101 BP.
 XX ID ADR61500;
 AC AC DT 02-DEC-2004 (first entry)
 CC Cotton cDNA sequence, SEQ ID 2281.
 DB XX Cotton, ss; plant; cold tolerance; growth rate; cell cycle pathway;
 KW drought tolerance; plant disease resistance; galactomannan; lignin;
 KW plant growth regulator; heat tolerance; herbicide tolerance;
 KW homologous recombination; extreme osmotic condition tolerance;
 KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
 KW stress resistance.
 XX OS Gossypium hirsutum.
 XX PN US2004181830-A1.
 XX PD 16-SEP-2004.
 XX PR 29-JAN-2004; 2004US-00767795.
 XX PR 07-MAY-2001; 2001US-00849529.
 XX PR 12-DEC-2001; 2001US-00021323.
 XX PA (KOVA/) KOVALIC D K.
 PA (ZHOU/) ZHOU Y.
 PA (CAO/) CAO Y.
 XX PI Kovalic DK, Zhou Y, Cao Y;
 XX DR WPI; 2004-667718/65.
 XX PT New recombinant nucleic acid molecules and polypeptides from Gossypium
 PT hirsutum, useful for producing plants with improved biological
 PT characteristics (e.g. improved plant cold or drought tolerance).
 XX PS Claim 1; SEQ ID NO 2281; 14pp; English.
 XX CC The invention relates to a recombinant polynucleotide comprising any of
 CC the 58758 Cotton plant DNA sequences mentioned in the specification.
 CC Also a recombinant polypeptide comprising any of the 58758 amino acid
 CC sequences mentioned in the specification and producing a plant having an
 CC improved property. Producing a plant having an improved property
 CC comprises transforming a plant with a recombinant construct comprising a
 CC promoter region functional in a plant cell operably joined to a
 CC polynucleotide comprising a coding sequence for a polypeptide associated
 CC with the property, and growing the transformed plant. The polypeptide is
 CC useful for improving plant cold tolerance, manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, improving plant
 CC drought tolerance, providing increased resistance to plant disease,
 CC producing galactomannan (or lignin or plant growth regulators), improving
 CC plant heat tolerance, improving plant tolerance to herbicides, increasing
 CC the rate of homologous recombination in plants, improving plant tolerance
 CC to extreme osmotic conditions or to pathogens or pests, improving yield
 CC by modification of photosynthesis, modifying seed oil or protein yield
 CC and/or content, improving yield by modification of carbohydrate, nitrogen
 CC or phosphorus use and/or uptake, or improving yield by providing improved
 CC plant growth and development under at least one stress condition. The
 CC polynucleotide and polypeptide may also be used in recombinant DNA
 CC constructs, in physical arrays of molecules, as plant breeding markers,
 CC or in computer-based storage and analysis systems. The present sequence

CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this CC patent did not form part of the printed specification, but was obtained CC in electronic format directly from USPTO at CC <http://uspto.gov/sequence.html?DocID=20040181830>. However only 6585 CC polynucleotide sequences were available, the remaining 52213 CC polynucleotides and all 58798 protein sequences were not present.

XX Sequence 1101 BP; 308 A; 201 C; 254 G; 338 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 13; Length 1101; Best Local Similarity 73.3%; Pred. No. 29; Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUGAGCUC 20
|:|:|:|:|:|:|:
Db 1027 CTCACCTCGTGAAGCTC 1041

RESULT 13

ABA14473 standard; DNA; 1191 BP.
ID ABA14473;

XX DT 23-JAN-2002 (first entry)

XX Human nervous system related polynucleotide SEQ ID NO 6804.

XX Human; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnear; anti-parkinsonian; antischikling; antianemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; anticonvulsant; antifungal; antiparasitic; cariant; immune disorder; cardiovascular disorder; KW antineoplastic; infection; nephrotropic; gene therapy; vaccine; ds. XX neurological disease; infection; nephrotropic; gene therapy; vaccine; ds. XX Homo sapiens.

OS WO200159063-A2.

PN XX

PD 16-AUG-2001.

XX XX 17-JAN-2001; 20011WO-US001334.

PR 31-JAN-2000; 2000US-0179065P.

PR 04-02-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-018635P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-019812P.

PR 19-NAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0208467P.

PR 28-JUN-2000; 2000US-02148P.

PR 30-JUL-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216547P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0222964P.

PR 14-AUG-2000; 2000US-0224567P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225457P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-022182P.
PR 23-AUG-2000; 2000US-022109P.
PR 30-AUG-2000; 2000US-022924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-022343P.
PR 01-SEP-2000; 2000US-022344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-02310437P.
PR 06-SEP-2000; 2000US-02310438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0231081P.
PR 08-SEP-2000; 2000US-0231143P.
PR 08-SEP-2000; 2000US-0231397P.
PR 14-SEP-2000; 2000US-0231398P.
PR 14-SEP-2000; 2000US-0231414P.
PR 14-SEP-2000; 2000US-0232080P.
PR 14-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0233399P.
PR 14-SEP-2000; 2000US-0234141P.
PR 14-SEP-2000; 2000US-0234201P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-02331064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-OCT-2000; 2000US-0234223P.
PR 21-OCT-2000; 2000US-0234274P.
PR 25-OCT-2000; 2000US-0234997P.
PR 25-OCT-2000; 2000US-0234998P.
PR 26-OCT-2000; 2000US-0235484P.
PR 27-OCT-2000; 2000US-0235834P.
PR 27-OCT-2000; 2000US-0235836P.
PR 29-OCT-2000; 2000US-0236327P.
PR 29-OCT-2000; 2000US-0236367P.
PR 29-OCT-2000; 2000US-0236368P.
PR 29-OCT-2000; 2000US-0236369P.
PR 02-OCT-2000; 2000US-023370P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-023710P.
PR 02-OCT-2000; 2000US-0237140P.
PR 13-OCT-2000; 2000US-023935P.
PR 13-OCT-2000; 2000US-023937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0242221P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-024617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.

XX Claim 25; SEQ ID NO 16153; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SNP).

CC The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.

XX Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;

Best Local Similarity 80.0%; Pred. No. 30;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACUGUGAGGCTT 22

Db 1774 CACTGTGAGCTT 1760

RESULT 18

ABA49335_C

ID ABA49335 standard; DNA; 1820 BP.

XX

AC ABA49335;

XX

DT 01-FEB-2002 (first entry)

XX Human breast cell single exon nucleic acid probe #8030.

DE Human; microarray; single exon probe; gene expression; breast; disease; cancer; ss.

KW

XX Homo sapiens.

OS

XX WO201015771-A2.

PN

XX 09-AUG-2001.

PD

XX 30-JAN-2001; 2001WO-US000662.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR

XX 26-MAY-2000; 2000US-0207456P.

PR

XX 30-JUN-2000; 2000US-0207456P.

PR

XX 03-AUG-2000; 2000US-00632366.

PR

XX 21-SEP-2000; 2000US-00632366.

PR

XX 27-SEP-2000; 2000US-0236359P.

PR

XX 04-OCT-2000; 2000US-0236359P.

PA

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI

XX Penn SG, Hanzel DK, Chen W, Rank DR;

DR

XX WPI; 2001-496933/54.

PT

XX New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.

PS

XX Claim 4; SEQ ID NO 8030; 327bp + Sequence Listing; English.

CC The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosis breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag

CC microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;

Best Local Similarity 80.0%; Pred. No. 30;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACUGUGAGGCTT 22

Db 1774 CACTGTGAGCTT 1760

RESULT 19

ABA34342_C

ID ABA34342 standard; DNA; 1820 BP.

XX

AC ABA34342;

XX

DT 23-JAN-2002 (first entry)

XX

DB Probe #12808 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.

KW

XX Homo sapiens.

OS

XX WO200157274-A2.

PN

XX 09-AUG-2001.

PD

XX 30-JAN-2001; 2001WO-US000666.

PF

XX 04-FEB-2000; 2000US-0180312P.

PR

XX 26-MAY-2000; 2000US-0207456P.

PR

XX 30-JUN-2000; 2000US-00632366.

PR

XX 03-AUG-2000; 2000US-00632366.

PR

XX 21-SEP-2000; 2000US-0236359P.

PR

XX 04-OCT-2000; 2000US-00024263.

PA

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI

XX Penn SG, Hanzel DK, Chen W, Rank DR;

DR

XX WPI; 2001-488899/53.

PT

XX Single exon nucleic acid probes for analyzing gene expression in human hearts.

PS

XX Claim 4; SEQ ID NO 12808; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and diagnosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)

SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;

Query Match 68.2%; Score 15; DB 4; Length 1820;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 AC XX
 DT 09-OCT-2001 (first entry)

DE XX
 KW Probe #7860 used to measure gene expression in human breast sample.
 KW Probe; human; breast disease; breast cancer; development disorder; ss;
 KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.
 KW XX
 OS Homo sapiens.
 PN WO200157270-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-US000661.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 21-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-476286/51.

XX
 PT Novel single exon nucleic acid probe used to measuring gene expression in a human breast.
 XX
 PT Claim 25; SEQ ID NO 7860; 322pp; English.
 XX
 CC The present invention relates to novel single exon nucleic acid probes.
 CC The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridizes at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic aetiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <http://wipo.int/patent/applications/search/pct>

CC SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;
 CC Query Match 68.2%; Score 15; DB 5; Length 1820;
 CC Best Local Similarity 80.0%; Pred. No. 30;
 CC Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 CC AC XX
 CC DT 19-AUG-2002 (first entry)
 CC DB XX
 CC KW Human genome-derived single exon probe ORF from lung SEQ ID No 15429.
 CC KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 CC KW chronic obstructive pulmonary disease; interstitial lung disease;
 CC KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

RESULT 21
 AA107869/C
 ID AA107869
 XX AA107869 standard; DNA; 1820 BP.

Query Match 68.2%; Score 15; DB 4; Length 1820;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 AC XX
 DT 19-AUG-2002 (first entry)

DB XX
 KW Human genome-derived single exon probe ORF from lung SEQ ID No 15429.
 KW Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
 KW chronic obstructive pulmonary disease; interstitial lung disease;
 KW familial idiopathic pulmonary fibrosis; neurofibromatosis;

tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
 KW Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
 KW pulmonary histiocytosis; lymphangioleiomytosis; Karagener syndrome;
 KW pulmonary alveolar proteinosis; fibrocytic pulmonary dysplasia;
 KW primary ciliary dyskinesia; pulmonary hypertension;
 KW pulmonary membrane disease; open reading frame; ORF.
 XX Homo sapiens.
 XX WO200186003-A2.
 PD 15-NOV-2001.
 PF 30-JAN-2001; 2001WO-US000665.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-02060808.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0234687P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX DR WPI; 2002-114183/15.
 XX PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX PS SEQ ID NO 15420; 63pp; English.
 XX The invention relates to a spatially-addressable set of single exon
 nucleic acid probes for measuring gene expression in a sample derived
 from human lung comprising single exon nucleic acid probes having one of
 12614 nucleic acid sequences mentioned in the specification, or their
 complements or the 12387 open reading frames derived from the 12614
 probes. Also included are a microarray comprising the novel set of probes
 ; the novel set of probes which hybridise at high stringency to a nucleic
 acid expressed in the human lung; measuring gene expression in a sample
 derived from human lung, comprising (a) contacting the array with a
 collection of detectably labelled nucleic acids derived from human lung
 mRNA, and (b) measuring the label detectably bound to each probe of the
 array; identifying exons in a eukaryotic genome, comprising (a)
 algorithmically predicting at least one exon from genomic sequences of
 the eukaryote; and (b) detecting specific hybridisation of detectably
 labelled nucleic acids from eukaryotic lung mRNA, to a single exon probe,
 having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning the label detectably bound to each probe of the
 array; identifying exons in a eukaryotic genome, comprising (a)
 algorithmically predicting at least one exon from genomic sequences of
 the eukaryote; and (b) detecting specific hybridisation of detectably
 labelled nucleic acids from eukaryotic lung mRNA, to a single exon probe,
 having a fragment identical to the predicted exon, the probe is included
 in the above mentioned microarray; assigning exons to a single gene,
 comprising (a) identifying exons from genomic sequence by the method
 above and (b) measuring the expression of each of the exons in several
 tissues and/or cell types using hybridisation to single exon
 microarrays having a probe with the exon, where a common pattern of
 expression of the exons in the tissues and/or cell types indicates that
 the exons should be assigned to a single gene; a peptide comprising one
 of 12011 sequences, mentioned in the specification, or encoded by the
 probes/open reading frames (ORF). The probes are used for gene expression
 analysis, and for identifying exons in a gene, particularly using human
 lung derived mRNA and for the study of lung diseases such as asthma, lung
 cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
 histiocytosis, lymphangioleiomytosis, pulmonary alveolar proteinosis,
 Karagener syndrome, fibrocytic pulmonary dysplasia, primary ciliary
 dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 present sequence is a single exon probe open reading frame of the
 invention. Note: The sequence data for this patent did not form part of
 the printed specification, but was obtained in electronic format directly
 from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1820 BP; 546 A; 406 C; 445 G; 423 T; 0 U; 0 Other;
 Query Match 68.2%; Score 15; DB 6; Length 1820;
 Best Local Similarity 80.0%; Pred. No. 30;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CACUUGUGGACCUCT 22
 DB 1774 CACTGTGAGCTCT 1760

RESULT 23
 AAI24124^C
 ID AAI24124 standard; DNA; 1870 BP.
 XX AAI24124 AC
 XX DT 12-OCT-2001 (first entry)
 XX DE Probe #14057 for gene expression analysis in human cervical cell sample.
 XX KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer; ss.
 XX OS Homo sapiens.
 XX PN WO200157278-A2.
 XX PD 09-AUG-2001.
 XX PP 30-JAN-2001; 2001WO-US000670.
 XX PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00632366.
 PR 03-AUG-2000; 2000US-00632366.
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 PR 27-SEP-2000; 2000US-0234687P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX PR 04-FEB-2000; 2000US-0180312P.
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 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
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 XX PA (MOLE-) MOLECULAR DYNAMICS INC.
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 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 20

RESULT 24
 ABA69247 /C
 ID ABA69247 standard; DNA; 1870 BP.
 XX
 AC ABA69247;
 XX
 DT 01-FEB-2002 (first entry)
 XX Human foetal liver single exon nucleic acid probe #17552.
 DE XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 XX
 OS Homo sapiens.
 XX WO200152277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PP 30-JAN-2001; 2001WO-US0006659.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
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 PR 30-JUN-2000; 2000US-00608408.
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 PR 21-SEP-2000; 2000US-023468P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000US-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488897/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human placenta.
 XX
 PR 27-SEP-2000; 2000US-0236359P.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483447/52.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 gene expression in human fetal liver.
 XX
 PS Claim 4; SEQ ID NO 17552; 639pp + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a single exon nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
 XX
 Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-023468P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000US-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.

RESULT 25
 AAI49420 /C
 ID AAI49420 standard; DNA; 1870 BP.
 XX
 AC AAI49420;
 XX
 DT 17-OCT-2001 (first entry)
 XX Probe #18106 used to measure gene expression in human placenta sample.
 DE XX
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder; ss.
 XX
 OS Homo sapiens.

XX	PI	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	XX	
XX	DR	
XX	WPI;	2001-496933/54.
XX	PT	
XX	PT	New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
XX	PS	Claim 4 ; SEQ ID NO 9934; 327pp + Sequence Listing; English.
XX	XX	The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarray. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	SQ	Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;
XX	XX	Query Match 68.2%; Score 15; DB 4; Length 1870; Best Local Similarity 80.0%; Pred. No. 30; Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX	XX	RESULT 27 ABA36163/C ID ABA36163 standard; DNA; 1870 BP. AC ABA36163;
XX	XX	23-JAN-2002 (first entry)
XX	XX	Probe #14629 for gene expression analysis in human heart cell sample.
XX	KW	Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
XX	KW	Homo sapiens.
XX	OS	WO200157274-A2.
XX	PN	09-AUG-2001.
XX	PD	30-JAN-2001; 2001IWO-US000666.
XX	PR	04-FEB-2000; 2000US-0180312P.
XX	PR	26-MAY-2000; 2000US-0207456P.
XX	PR	30-JUN-2000; 2000US-00608408.
XX	PR	03-AUG-2000; 2000US-00632366.
XX	PR	21-SEP-2000; 2000US-0234687P.
XX	PR	27-SEP-2000; 2000US-0234659P.
XX	PR	04-OCT-2000; 2000GB-00024263.
XX	PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	XX	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	XX	WPI; 2001-488999/53.
XX	PT	Single exon nucleic acid probes for analyzing gene expression in human heart.
XX	PS	Claim 4 ; SEQ ID NO 14629; 530pp; English.
XX	XX	The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosis diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	SQ	Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;
XX	XX	Query Match 68.2%; Score 15; DB 4; Length 1870; Best Local Similarity 80.0%; Pred. No. 30; Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX	XX	Qy 8 CACUCUGAGCTT 22 Db 1774 CACTCGTAGCTT 1760
XX	XX	RESULT 28 AAK43349/C ID AAK43349 standard; DNA; 1870 BP. AC AAK43349; XX DT 06-NOV-2001 (first entry)
XX	XX	Human bone marrow expressed single exon probe SEQ ID NO: 17906.
XX	DB	Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
XX	XX	Homosapiens.
XX	XX	W0200157276-A2.
XX	XX	09-AUG-2001.
XX	XX	30-JAN-2001; 2001IWO-US000668.
XX	XX	04-FEB-2000; 2000US-0180312P.
XX	XX	26-MAY-2000; 2000US-0207456P.
XX	XX	30-JUN-2000; 2000US-00608408.
XX	XX	03-AUG-2000; 2000US-00632366.
XX	XX	21-SEP-2000; 2000US-0234687P.
XX	XX	27-SEP-2000; 2000US-0234659P.
XX	XX	04-OCT-2000; 2000GB-00024263.
XX	PA	(MOLE-) MOLECULAR DYNAMICS INC.
XX	XX	Penn SG, Hanzel DK, Chen W, Rank DR;
XX	XX	WPI; 2001-488900/53.
XX	PT	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
XX	PS	Example 4 ; SEQ ID NO 17906; 658pp + Sequence Listing; English.
XX	XX	The present invention provides a number of single exon nucleic acid

probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention

XX Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;

SQ Query Match 68.2%; Score 15; DB 4; Length 1870;

Best Local Similarity 80.0%; Pred. No. 30;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACUGUGGAGCUCTT 22

Db 1774 CACUGUGGAGCUCTT 1760

Query Match 68.2%; Score 15; DB 4; Length 1870;

Best Local Similarity 80.0%; Pred. No. 30;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACUGUGGAGCUCTT 22

Db 1774 CACUGUGGAGCUCTT 1760

Query Match 68.2%; Score 15; DB 4; Length 1870;

Best Local Similarity 80.0%; Pred. No. 30;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACUGUGGAGCUCTT 22

Db 1774 CACUGUGGAGCUCTT 1760

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Query Match 68.2%; Score 15; DB 4; Length 1870;

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Best Local Similarity 80.0%; Pred. No. 30;

Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACUGUGGAGCUCTT 22

RESULT 30

ABS17430/C

ID ABS17430

XX ABS17430;

XX 19-AUG-2002 (first entry)

XX Human genome-derived single exon probe ORF from lung SEQ ID No 17421.

XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;

XX chronic obstructive pulmonary disease; interstitial lung disease;

XX familial idiopathic pulmonary fibrosis; neurofibromatosis;

XX tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;

XX Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;

XX pulmonary histiocytosis; lymphangiomyomatosis; Kartagener syndrome;

XX primary ciliary dyskinesia; pulmonary hypertension; fibrocytic pulmonary

XX hyaline membrane disease; open reading frame; ORF.

XX Homo sapiens.

XX WO20010186003-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000667.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX PI 2001-483446/52.

XX Single exon nucleic acid probes for analyzing gene expression in human

XX brains.

XX Example 4: SEQ ID NO 17532; 650pp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

XX probes which are derived from genomic sequences expressed in the human

XX brain. They can be used to measure gene expression in brain cell samples,

XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is one of the probes of the

XX invention

XX Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;

XX WOPI: 2001-483446/52.

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XX which may enable the diagnosis and improved treatment of nervous system

XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

XX epilepsy and cancers. The present sequence is one of the probes of the

CC the exons should be assigned to a single gene; a peptide comprising one
CC of 1201 sequences, mentioned in the specification, or encoded by the
CC probes/open reading frames (ORF). The probes are used for gene expression
CC analysis, and for identifying exons in a gene, particularly using human
CC lung derived mRNA and for the study of lung diseases such as asthma, lung
CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
CC Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary
CC histiocytosis, lymphangiomyomatosis, pulmonary alveolar proteinosis,
CC Kartagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary
CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
CC present sequence is a single exon probe open reading frame of the
CC invention. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp://ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1870 BP; 568 A; 416 C; 455 G; 431 T; 0 U; 0 Other;

SQ Query Match 68.2%; Score 15; DB 6; Length 1870;
Best Local Similarity 80.0%; Pred. No. 30;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CACUUGUGAGCUU 22
|||:|||:|||:|||:
Db 1774 CACTGGTGAAGCTCTT 1760

Search completed: July 20, 2005, 23:34:20
Job time : 455 secs

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OM nucleic - nucleic search, using sw model

Run on: July 20, 2005, 22:37:01 ; Search time 3090 Seconds

(without alignments)
 271.008 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugaaucacucugcugaggcucc 22

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 300 summaries

Database : EST:*

1: 9b_est1:*

2: 9b_est2:*

3: 9b_hnc:*

4: 9b_est3:*

5: 9b_est4:*

6: 9b_est5:*

7: 9b_est6:*

8: 9b_gss1:*

9: 9b_gss2:*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
C 1	17	77.3	1344	4	BG917388	602816903	CG989001 30DGS-06
C 2	16	72.7	200	7	CF296001	CF299826 7LEAF--04	CF298930 7LEAF--02
C 3	16	72.7	206	7	CF298930	CF298930 7LEAF--04	CF298930 7LEAF--02
C 4	16	72.7	245	7	CF298930	CF298930 7LEAF--04	CF298930 7LEAF--02
C 5	16	72.7	270	2	BE228712	BE228712 98AS025	CF298930 7LEAF--04
C 6	16	72.7	272	7	CF295034	CF295034 30DGS-04	CF295034 30DGS-04
C 7	16	72.7	273	7	CF299062	CF299062 7LEAF--02	CF299062 7LEAF--02
C 8	16	72.7	273	7	CF300491	CF300491 7LEAF--04	CF300491 7LEAF--04
C 9	16	72.7	276	7	CF300259	CF300259 7LEAF--04	CF300259 7LEAF--04
C 10	16	72.7	277	7	CF298981	CF298981 7LEAF--02	CF298981 7LEAF--02
C 11	16	72.7	281	7	CF298936	CF298936 7LEAF--01	CF298936 7LEAF--01
C 12	16	72.7	283	7	CF294911	CF294911 30DGS-04	CF294911 30DGS-04
C 13	16	72.7	311	7	CF299992	CF299992 7LEAF--04	CF299992 7LEAF--04
C 14	16	72.7	313	6	CB668095	CB668095 OSNED15M	CB668095 OSNED15M
C 15	16	72.7	315	7	CF300735	CF300735 7LEAF--05	CF300735 7LEAF--05
C 16	16	72.7	321	7	CF300267	CF300267 7LEAF--04	CF300267 7LEAF--04
C 17	16	72.7	321	7	CF334972	CF334972 JMT--04-H	CF334972 JMT--04-H
C 18	16	72.7	324	7	CF301775	CF301775 7LEAF--06	CF301775 7LEAF--06
C 19	16	72.7	326	7	CF295032	CF295032 30DGS-04	CF295032 30DGS-04
C 20	16	72.7	326	7	CF300479	CF300479 7LEAF--04	CF300479 7LEAF--04
C 21	16	72.7	329	7	CF298299	CF298299 7LEAF--06	CF298299 7LEAF--06
C 22	16	72.7	330	7	CF301705	CF301705 7LEAF--06	CF301705 7LEAF--06
C 23	16	72.7	340	7	CF299101	CF299101 7LEAF--02	CF299101 7LEAF--02
C 24	16	72.7	342	7	CF294601	CF294601 30DGS-04	CF294601 30DGS-04

C 25	16	72.7	343	7	CF300860	CF300860 7LEAF--05	CF300860 7LEAF--05
C 26	16	72.7	349	4	CF3022308	CF3022308 7LEAF--04	CF3022308 7LEAF--04
C 27	16	72.7	350	4	BI1810487	BI1810487 JMT--03-O	BI1810487 JMT--03-O
C 28	16	72.7	350	7	CF333339	CF333339 JMT--03-A	CF333339 JMT--03-A
C 29	16	72.7	351	7	CF300157	CF300157 7LEAF--04	CF300157 7LEAF--04
C 30	16	72.7	352	7	CF301559	CF301559 7LEAF--05	CF301559 7LEAF--05
C 31	16	72.7	353	7	CF294542	CF294542 30DGS-04	CF294542 30DGS-04
C 32	16	72.7	358	7	CF293314	CF293314 30DGS-04	CF293314 30DGS-04
C 33	16	72.7	358	7	CF301446	CF301446 7LEAF--05	CF301446 7LEAF--05
C 34	16	72.7	359	7	CF301225	CF301225 30DGS-04	CF301225 30DGS-04
C 35	16	72.7	360	7	CF295099	CF295099 30DGS-04	CF295099 30DGS-04
C 36	16	72.7	361	7	CF293177	CF293177 30DGS-04	CF293177 30DGS-04
C 37	16	72.7	361	7	CF333477	CF333477 JMT--02-O	CF333477 JMT--02-O
C 38	16	72.7	363	7	CF294625	CF294625 30DGS-04	CF294625 30DGS-04
C 39	16	72.7	364	4	BI797027	BI797027 H062C08 E	BI797027 H062C08 E
C 40	16	72.7	364	7	CF294149	CF294149 30DGS-04	CF294149 30DGS-04
C 41	16	72.7	364	7	CF300473	CF300473 7LEAF--04	CF300473 7LEAF--04
C 42	16	72.7	365	7	CF302440	CF302440 7LEAF--08	CF302440 7LEAF--08
C 43	16	72.7	366	7	CF300889	CF300889 7LEAF--04	CF300889 7LEAF--04
C 44	16	72.7	367	7	CF334002	CF334002 JMT--03-C	CF334002 JMT--03-C
C 45	16	72.7	368	7	CF293465	CF293465 30DGS--02	CF293465 30DGS--02
C 46	16	72.7	368	7	CF294328	CF294328 30DGS--04	CF294328 30DGS--04
C 47	16	72.7	369	7	CF294197	CF294197 30DGS--04	CF294197 30DGS--04
C 48	16	72.7	372	7	CF334668	CF334668 JMT--04-A	CF334668 JMT--04-A
C 49	16	72.7	373	7	CF298519	CF298519 7LEAF--04	CF298519 7LEAF--04
C 50	16	72.7	373	7	CF299944	CF299944 7LEAF--04	CF299944 7LEAF--04
C 51	16	72.7	381	7	CF301512	CF301512 7LEAF--06	CF301512 7LEAF--06
C 52	16	72.7	382	6	CA882915	CA882915 SSHD19 RI	CA882915 SSHD19 RI
C 53	16	72.7	388	7	CF333248	CF333248 JMT--02-B	CF333248 JMT--02-B
C 54	16	72.7	389	2	BB228607	BB228607 9AS2665	BB228607 9AS2665
C 55	16	72.7	390	7	CF296172	CF296172 30DGS--06	CF296172 30DGS--06
C 56	16	72.7	389	7	CF302115	CF302115 7LEAF--07	CF302115 7LEAF--07
C 57	16	72.7	391	7	CF279865	CF279865 14ETL--06	CF279865 14ETL--06
C 58	16	72.7	394	7	CF292228	CF292228 30DGS--01	CF292228 30DGS--01
C 59	16	72.7	396	7	CF294499	CF294499 30DGS--02	CF294499 30DGS--02
C 60	16	72.7	397	7	CF295574	CF295574 30DGS--05	CF295574 30DGS--05
C 61	16	72.7	398	7	CF281031	CF281031 14ETL--07	CF281031 14ETL--07
C 62	16	72.7	400	7	CF293653	CF293653 30DGS--02	CF293653 30DGS--02
C 63	16	72.7	400	7	CF301091	CF301091 7LEAF--05	CF301091 7LEAF--05
C 64	16	72.7	402	7	CF292298	CF292298 30DGS--01	CF292298 30DGS--01
C 65	16	72.7	402	7	CF301882	CF301882 7LEAF--05	CF301882 7LEAF--05
C 66	16	72.7	402	7	CF333799	CF333799 JMT--02-N	CF333799 JMT--02-N
C 67	16	72.7	404	7	CF293371	CF293371 30DGS--02	CF293371 30DGS--02
C 68	16	72.7	405	7	CF292038	CF292038 14ROOT--00	CF292038 14ROOT--00
C 69	16	72.7	406	7	CF291160	CF291160 14ROOT--00	CF291160 14ROOT--00
C 70	16	72.7	407	7	CF295556	CF295556 30DGS--06	CF295556 30DGS--06
C 71	16	72.7	409	7	CF297322	CF297322 30DGS--08	CF297322 30DGS--08
C 72	16	72.7	412	7	CF302167	CF302167 7LEAF--07	CF302167 7LEAF--07
C 73	16	72.7	414	7	CF292334	CF292334 30DGS--01	CF292334 30DGS--01
C 74	16	72.7	415	7	CF292393	CF292393 30DGS--01	CF292393 30DGS--01
C 75	16	72.7	415	7	CF317419	CF317419 HD--07-B1	CF317419 HD--07-B1
C 76	16	72.7	417	7	CF302441	CF302441 7LEAF--08	CF302441 7LEAF--08
C 77	16	72.7	417	7	CF3337043	CF3337043 JMT--07-F	CF3337043 JMT--07-F
C 78	16	72.7	419	7	CF310192	CF310192 ABF--04-L	CF310192 ABF--04-L
C 79	16	72.7	420	6	CA752317	CA752317 JSYL446 R	CA752317 JSYL446 R
C 80	16	72.7	420	6	CA752323	CA752323 JSYL471 R	CA752323 JSYL471 R
C 81	16	72.7	421	6	CA755899	CA755899 JSYL374 R	CA755899 JSYL374 R
C 82	16	72.7	421	7	CF291078	CF291078 30DGS--02	CF291078 30DGS--02
C 83	16	72.7	423	7	CF301435	CF301435 7LEAF--06	CF301435 7LEAF--06
C 84	16	72.7	424	2	AW065961	AW065961 mgie1002A	AW065961 mgie1002A
C 85	16	72.7	424	2	CF295077	CF295077 30DGS--04	CF295077 30DGS--04
C 86	16	72.7	427	7	CF335603	CF335603 JMT--05-F	CF335603 JMT--05-F
C 87	16	72.7	427	7	CF300999	CF300999 7LEAF--04	CF300999 7LEAF--04
C 88	16	72.7	428	7	CF302576	CF302576 7LEAF--08	CF302576 7LEAF--08
C 89	16	72.7	428	7	CF301452	CF301452 7LEAF--06	CF301452 7LEAF--06
C 90	16	72.7	431	7	CF293115	CF293115 30DGS--02	CF293115 30DGS--02
C 91	16	72.7	431	7	CF295077	CF295077 30DGS--04	CF295077 30DGS--04
C 92	16	72.7	431	7	CF293108	CF293108 30DGS--02	CF293108 30DGS--02
C 93	16	72.7	433	7	CF299230	CF299230 30DGS--03	CF299230 30DGS--03
C 94	16	72.7	433	7	CF299231	CF299231 7LEAF--03	CF299231 7LEAF--03
C 95	16	72.7	434	4	BM038487	BM038487 100210 O	BM038487 100210 O
C 96	16	72.7	435	4	BI795494	BI795494 H023107 O	BI795494 H023107 O
C 97	16	72.7	435	7	CP297684	CP297684 30DGS--08	CP297684 30DGS--08
C 98	16	72.7	436	7	CF333485	CF333485 JMT--02-G	CF333485 JMT--02-G

C 98	16	72.7	437	7	CF300287	7LEAF--04	CF335971	JMT--05-N
C 99	16	72.7	438	7	CF335757	JMT--06-0	CF35871	JMT--05-L
C 100	16	72.7	439	7	CF336454	JMT--06-1	CF302098	7LEAF--07
C 101	16	72.7	440	4	BI81469	J009B04 O	CF336032	JMT--05-P
C 102	16	72.7	443	7	CF298634	7LEAF--02	CF294456	30DGS--03
C 103	16	72.7	443	7	CF326605	JMT1--06-	CF201786	7LEAF--06
C 104	16	72.7	444	7	CF296710	0DGS--07	CF356909	JMT--07-C
C 105	16	72.7	447	7	CF300126	7LEAF--04	CF222748	30DGS--04
C 106	16	72.7	447	7	CF334006	JMT--03-C	CF2994949	7LEAF--04
C 107	16	72.7	447	7	CF335012	JMT--04-1	CF36522	JMT--06-J
C 108	16	72.7	448	7	CF298622	30DGS--01	CF300189	7LEAF--03
C 109	16	72.7	448	7	CF298719	7LEAF--02	CF302481	7LEAF--04
C 110	16	72.7	452	7	CF299236	7LEAF--03	CF35479	JMT--05-C
C 111	16	72.7	454	7	CF307856	ABF--01-H	CF294477	30DGS--04
C 112	16	72.7	455	7	CF298335	7LEAF--01	CF297419	30DGS--08
C 113	16	72.7	455	7	CF334345	JMT--02-F	CF299486	P007C11 O
C 114	16	72.7	459	7	CF298381	30DGS--05	CF296926	30DGS--07
C 115	16	72.7	459	7	CF302341	7LEAF--07	CF30189	7LEAF--04
C 116	16	72.7	460	4	BI805959	A006C09 O	CF335479	JMT--05-C
C 117	16	72.7	461	7	CF193895	Azb12.1	CF32788	JMT--01-G
C 118	16	72.7	461	7	CF311539	ABF--01-H	CF329442	JMT--01-K
C 119	16	72.7	462	7	CF295701	30DGS--05	CF335956	JMT--05-N
C 120	16	72.7	462	7	CF297362	30DGS--05	CF36502	JMT--06-J
C 121	16	72.7	462	7	CF299260	7LEAF--03	CF293284	30DGS--02
C 122	16	72.7	463	7	CF295676	30DGS--05	CF300694	7LEAF--03
C 123	16	72.7	464	7	CF290755	30DGS--04	CF334025	JMT--03-C
C 124	16	72.7	464	7	CF298102	7LEAF--01	CF34152	JMT--03-F
C 125	16	72.7	466	7	CF333098	JMT--01-N	CF335291	JMT--04-O
C 126	16	72.7	466	7	CF36355	JMT--06-G	CF335956	JMT--05-M
C 127	16	72.7	467	7	CF295382	30DGS--05	CF295778	h12-t3.8E
C 128	16	72.7	467	7	CF298470	7LEAF--03	CF333698	JMT--02-L
C 129	16	72.7	467	7	CF332819	JMT--01-H	CF208990	ABF--03-A
C 130	16	72.7	467	7	CF298102	JMT--08-L	CF346371	JMT--06-G
C 131	16	72.7	469	7	CF300208	7LEAF--01	CF302471	7LEAF--08
C 132	16	72.7	470	7	CF298227	7LEAF--01	CF312560	ABF--08-F
C 133	16	72.7	470	7	CF302203	7LEAF--07	CF337598	JMT--08-P
C 134	16	72.7	472	7	CF297460	30DGS--08	CF753360	ABF--03-A
C 135	16	72.7	472	7	CF29893	7LEAF--04	CF2957567	P008G11 O
C 136	16	72.7	472	7	CF336041	JMT--02-H	CF301004	7LEAF--04
C 137	16	72.7	473	7	CF334916	JMT--04-G	CF353313	JMT--04-P
C 138	16	72.7	474	7	CF311574	ABF--06-N	CF312560	ABF--08-F
C 139	16	72.7	474	7	CF334359	JMT--03-K	CF296585	30DGS--07
C 140	16	72.7	474	7	CF335615	JMT--05-F	AA733360	ABF--02-B
C 141	16	72.7	474	7	BI807979	G003A04 O	CF2975579	30DGS--05
C 142	16	72.7	475	7	CF333611	JMT--02-D	CF302633	JMT--04-P
C 143	16	72.7	475	7	CF34916	JMT--04-G	CF335313	JMT--04-P
C 144	16	72.7	475	7	CF311574	ABF--06-N	CF327248	JMT--07-J
C 145	16	72.7	475	7	CF334359	JMT--03-K	CF296585	30DGS--07
C 146	16	72.7	480	4	BM419049	R008F02 O	CF333254	JMT--02-B
C 147	16	72.7	480	7	CF331227	JMT--01-O	CF336913	JMT--07-C
C 148	16	72.7	481	7	CF332849	ABF--08-M	CF295579	30DGS--05
C 149	16	72.7	481	7	CF336043	JMT--08-L	CF340479	JMT--03-D
C 150	16	72.7	481	7	BF431561	OG02C02T3	CF33590	JMT--02-I
C 151	16	72.7	484	7	CF302933	7LEAF--08	CF334927	JMT--04-G
C 152	16	72.7	484	7	CF334479	JMT--03-M	CF312061	ABF--07-E
C 153	16	72.7	484	7	CF333350	JMT--04-P	CF333207	JMT--02-A
C 154	16	72.7	485	7	CF30641	7LEAF--08	CF36446	JMT--06-I
C 155	16	72.7	485	7	CF336484	JMT--06-I	CF229988	99AS225 R
C 156	16	72.7	486	7	CF298252	30DGS--05	CF300116	7LEAF--04
C 157	16	72.7	486	7	CF297412	30DGS--08	CF37862	JMT--08-H
C 158	16	72.7	486	7	CF298637	7LEAF--03	CF37639	JMT--08-C
C 159	16	72.7	486	7	CF336999	JMT--07-B	CF294297	30DGS--03
C 160	16	72.7	486	7	CF337803	JMT--08-G	CF297126	30DGS--02
C 161	16	72.7	487	7	CF30594	7LEAF--08	CF299626	7LEAF--03
C 162	16	72.7	487	7	CF332798	JMT--01-H	CF36924	JMT--07-C
C 163	16	72.7	487	7	CF334015	JMT--03-C	CF295780	30DGS--05
C 164	16	72.7	487	7	CF332223	JMT--04-N	CF29889	7LEAF--08
C 165	16	72.7	487	7	CF335874	JMT--05-L	CR286903	CR286903
C 166	16	72.7	487	7	CF335893	JMT--05-L	CF29884	7LEAF--02
C 167	16	72.7	488	7	CF333761	JMT--02-M	CF337361	JMT--07-M
C 168	16	72.7	488	7	CF334521	JMT--03-N	CF332599	JMT--01-C
C 169	16	72.7	490	7	CF24832	30DGS--04	BM419793	R018G12 O
C 170	16	72.7	490	7	CF335453	JMT--05-C	BM419601	R016B01 O

/cultivar="Nackdong"
 /db_xref="taxon.39947"
 /clones="300GS-06-C24"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGSI)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN
 Query Match 72.7%; Score 16; DB 7; Length 200;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 6 CUCACUGGAGCT 21
 [:|:|:|:|:|:|:|:
 Db 107 CTCACCTGAGCTCT 92

RESULT 3
 CF299826/c
 LOCUS CF299826 206 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF-04-A01.g1 Rice leaf plasmid cDNA library II (7LEAF) *Oryza sativa* (japonica cultivar-group) cDNA clone 7LEAF-04-A01, mRNA sequence.
 ACCESSION CF299826
 VERSION 1
 KEYWORDS EST
 SOURCE *Oryza sativa* (japonica cultivar-group)
 ORGANISM *Oryza sativa* (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Orzyeae; *Oryza*.
 REFERENCE 1 (bases 1 to 245)
 AUTHORS Kim, J.S.; Jun, K.M.; Cheong, P.J.; Kim, M.J.; Lee, T.H.; Shin, Y.C.; Song, S.I.; Kim, J.K.; Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyunggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 322 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
 1..245
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clone="7LEAF-04-A01"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_id="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 ORIGIN
 Query Match 72.7%; Score 16; DB 7; Length 245;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 CUCACUGGAGCT 21
 [:|:|:|:|:|:|:
 Db 133 CTCACCTGAGCTCT 118

RESULT 5
 BE228712
 LOCUS 98AS025 Rice Immature Seed Lambda ZAPII cDNA Library *Oryza sativa* (indica cultivar-group)
 DEFINITION cDNA clone 98AS3025, mRNA sequence.
 ACCESSION BE228712
 VERSION BE228712.1
 KEYWORDS EST
 SOURCE *Oryza sativa* (indica cultivar-group)
 ORGANISM *Oryza sativa* (indica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Orzyeae; *Oryza*.
 REFERENCE 1 (bases 1 to 270)
 AUTHORS Nahm B.H.; Kim, J.K.; Cheong, J.J.; Kim, S.I.; Hahn, T.R.; Moon, E.P.; Kim, W.T.; Kim, W.Y.; Yang, M.S.; Park, R.D.; Sohn, U.I.; Kang, K.Y.; Lee, M.C. and Eun, M.Y.
 TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
 JOURNAL Unpublished (1998)
 COMMENT Department of Cytogenetics
 National Inst. of Agri. Sci. and Tech, RDA
 Suwon, Kyunggi, Korea

RESULT 4
 Query Match 72.7%; Score 16; DB 7; Length 206;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 CUCACUGGAGCT 21
 [:|:|:|:|:|:
 Db 106 CTCACCTGAGCTCT 91

FEATURES	Source	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47	6 CUCACUCUGAGGAGCT 21 : : : : : 129 CTCACTCGTCGAGCTCT 114	QY 6 CUCACUCUGAGGAGCT 21 : : : Db 129 CTCACTCGTCGAGCTCT 114
ORIGIN		RESULT 7 CF295062/c LOCUS DEFINITION SEQUENCE ACCESSION VERSION KEYWORDS ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCE	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47
FEATURES	Source	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47	6 CUCACUCUGAGGAGCT 21 : : : : : 129 CTCACTCGTCGAGCTCT 114	QY 6 CUCACUCUGAGGAGCT 21 : : : Db 129 CTCACTCGTCGAGCTCT 114
ORIGIN		RESULT 6 CF295034/c LOCUS DEFINITION SEQUENCE ACCESSION VERSION KEYWORDS ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCE	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47
FEATURES	Source	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47	6 CUCACUCUGAGGAGCT 21 : : : : : 129 CTCACTCGTCGAGCTCT 114	QY 6 CUCACUCUGAGGAGCT 21 : : : Db 129 CTCACTCGTCGAGCTCT 114
ORIGIN		RESULT 8 CP300491/c LOCUS DEFINITION SEQUENCE ACCESSION VERSION KEYWORDS ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCE	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47	Query Match Best Local Similarity 72.7%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; Db 32 CTCACTCGTCGAGCTCT 47

with oligoribonucleotides and then used as templates for RT-PCR."

FEATURES

ORIGIN

Query Match 72.7%; Score 16; DB 7; Length 276;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGGAGCCT 21
Db 264 CTCACTCGAGCTCT 249

ORIGIN

RESULT 10
CP298981/c
LOCUS CF298981
DEFINITION 7LEAF--02-L24.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-L24, mRNA sequence.

ACCESSION CF298981
VERSION GI:33670742
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryzae.

REFERENCE 1 (bases 1 to 277)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gabio.com, bhnahm@bio.myongji.ac.kr.

ORIGIN

Query Match 72.7%; Score 16; DB 7; Length 273;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGGAGCCT 21
Db 264 CTCACTCGAGCTCT 249

ORIGIN

RESULT 9
CP000259/c
LOCUS CF300259
DEFINITION 7LEAF--04-J11.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--04-J11, mRNA sequence.

ACCESSION CP300259
VERSION GI:33672200
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzeae; Oryzae.

REFERENCE 1 (bases 1 to 276)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K., and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gabio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

ORIGIN

Query Match 72.7%; Score 16; DB 7; Length 277;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGGAGCCT 21
Db 135 CTCACTCGAGCTCT 120

ORIGIN

RESULT 11
CP298536/c
LOCUS CP298536
DEFINITION 7LEAF--01-P09.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--01-P09, mRNA sequence.

ACCESSION CP298536
VERSION GI:33670297
KEYWORDS EST.

SOURCE ORYZA SATIVA (JAPONICA CULTIVAR-GROUP)

ORGANISM ORYZA SATIVA (JAPONICA CULTIVAR-GROUP) Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poales; Poaceae; Spermatophytina; Magnoliophyta; Liliopsida; Oryzae; Oryzae;

REFERENCE 1 (bases 1 to 281)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahn@gpbi.com, bhnahn@bio.myongji.ac.kr.

FEATURES source

1 .281

/organism="Oryza sativa (japonica cultivar-group)"

/mol type="mRNA"

/cultivar="Nackdong"

/db xref="taxon:39947"

/clone="7LEAF--01-P09"

/issue type="leaf"

/dev stage="7" days after germination"

/lab host="E.coli DH10B"

/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."

ORIGIN

RESULT 12

Query Match Score 16; DB 7; Length 281;

Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGAGCT 21

Db 1:||||:||||:||||:||| 115 CTCACTCGAGCT 100

LOCUS CF294911

DEFINITION 283 bp mRNA linear EST 14-AUG-2003

ORGANISM sativa (japonica cultivar-group) CDNA clone 30DGS-04-J322, mRNA sequence.

ACCESSION CF294911.1

VERSION GI:336633944

KEYWORDS EST.

ORGANISM ORYZA SATIVA (JAPONICA CULTIVAR-GROUP) Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Poales; Poaceae; Spermatophytina; Magnoliophyta; Liliopsida; Oryzae; Oryzae;

REFERENCE 1 (bases 1 to 283)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahn@gpbi.com, bhnahn@bio.myongji.ac.kr.

FEATURES source

1 .283

/organism="Oryza sativa (japonica cultivar-group)"

/mol type="mRNA"

/cultivar="Nackdong"

ORIGIN

Query Match Score 16; DB 7; Length 311;

Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGAGCT 21

Db 1:||||:||||:||||:||| 293 CTCACTCGAGCT 278

RESULT 14

CB668085

LOCUS CB668085 313 bp mRNA linear EST 09-APR-2003 COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division DEFINITION OSNED15M06_f OSNED15M06_5, mRNA sequence of Bioscience and Bioinformatics, MyongJi University

ACCESSION CB668085 GI:29671810 FEATURES source

KEYWORDS EST. Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

SOURCE ORGANISM *Oryza sativa* (japonica cultivar-group) Location/Qualifiers

1. .315 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong"

1. (bases 1 to 313) /db_xref="Taxon:39947" /clone="7LEAF--05-F05" /tissue_type="Leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."

REFERENCE AUTHORS Jantsburuyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. TITLE Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

JOURNAL COMMENT Unpublished (2003) Contact: Rod Wing Arizona Genomics Institute

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA

Te: 520 626 3967 Fax: 520 621 9288 Email: <http://genome.arizona.edu>

PCR PRIMERS FORWARD: gta aaa cga cgg cca gta g BACKWARD: gta aac aca tat gac cat g Plate: 15 row: M column: 06 Seq primer: gta aaa cga cgg cca gtg.

FEATURES source Location/Qualifiers

1. .313 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nipponbare" /db_xref="Taxon:39947" /clone="OSNED15M06" /tissue_type="Leaf" /dev_stage="3 week" /lab_host="DH10B" /clone_lib="OSNED" /note="Vector: PBBlueScript II KS+; Site 1: EcoRI; Site 2: XbaI; 24 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN Query Match Score 16; DB 6; Length 313; Best Local Similarity 75.0%; Pred. No. 37; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0; ORIGIN

1. (bases 1 to 321) /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong"

1. (bases 1 to 321) /db_xref="Taxon:39947" /clone="7LEAF--04-J16" /tissue_type="Leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."

REFERENCE AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nam,B.H. TITLE Large-scale Sequencing Analysis of Rice ESTs JOURNAL Unpublished (2003)

FEATURES source

1. .321 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nackdong"

1. (bases 1 to 321) /db_xref="Taxon:39947" /clone="7LEAF--04-J16" /tissue_type="Leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."

REFERENCE AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H. TITLE Large-scale Sequencing Analysis of Rice ESTs JOURNAL Unpublished (2003)

ORIGIN

/clone="30DGs--04-N22"
 /tissue type="leaf"
 /dev stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf Plasmid cDNA library I (30DGs)"
 /note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."
ORIGIN

Query Match 72.7%; Score 16; DB 7; Length 326;
 Best Local Similarity 75.0%; Pred. No. 37; Indels 0; Gaps 0;
 Matches 12; Conservative 4; Mismatches 0;
 ORY 6 CUCACUCGGAGGCTCT 21
 Db 308 CTCACCTCGAGGCTCT 293

RESULT 20
 CF00479/c
LOCUS CF300479 326 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-017.g1 Rice leaf plasmid cDNA library II (7LEAF) *Oryza sativa* (*japonica* cultivar-group) cDNA clone 7LEAF--04-017, mRNA sequence.
ACCESSION CF300479
VERSION 1
KEYWORDS EST.
ORGANISM *Oryza sativa* (*japonica* cultivar-group)
Oryza sativa (*japonica* cultivar-group)
Eukaryota; *Viridiplantae*; *Streptophytina*; *Embryophytina*; *Tracheophytina*; *Ehrhartiidae; *Oryza*.
REFERENCE 1 (bases 1 to 326)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyunggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.*

FEATURES source
 1..329
 /organism="Oryza sativa" (japonica cultivar-group)
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:39947"
 /clones="7LEAF--01-K01"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf Plasmid cDNA library II (7LEAF)"
 /note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with Oligoribonucleotides and then used as templates for RT-PCR."
ORIGIN

Query Match 72.7%; Score 16; DB 7; Length 326;
 Best Local Similarity 75.0%; Pred. No. 37; Indels 0; Gaps 0;
 Matches 12; Conservative 4; Mismatches 0;
 ORY 6 CUCACUCGGAGGCTCT 21
 Db 311 CTCACCTCGAGGCTCT 296

RESULT 22
 CF301705/c
LOCUS CF301705 330 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--06-K17.g1 Rice leaf plasmid cDNA library II (7LEAF) *Oryza sativa* (*japonica* cultivar-group) cDNA clone 7LEAF--06-K17, mRNA sequence.
ACCESSION CF301705
VERSION 1
KEYWORDS EST.
ORGANISM *Oryza sativa* (*japonica* cultivar-group)
Eukaryota; *Viridiplantae*; *Streptophytina*; *Embryophytina*; *Tracheophytina*; *Ehrhartiidae; *Oryza*.
REFERENCE 1 (bases 1 to 330)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K., and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University
 Yongin, Kyunggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355*

RESULT 21
 CF98299/c
LOCUS CF298299 329 bp mRNA linear EST 15-AUG-2003

FEATURES source Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr.
 1. .330 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="MacKdougall"
 /db_xref="taxon:39947"
 /clone="7LEAF-06-K17"
 /tissue_type="leaf"
 /dev_stage="7 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 ORIGIN
 Query Match 72.7%; Score 16; DB 7; Length 330;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 CUCACUCGAGCUCT 21
 Db 321 CTCACCTGGAGCTCT 306
 RESULT 23
 CF299101/C 340 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF--02-P10.91 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--02-P10, mRNA sequence.
 ACCESSION CF299101
 VERSION EST
 KEYWORDS SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poaceae;
 Bhrhartoidea; Orzyeae; Orzya.
 REFERENCE 1 (bases 1 to 342)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 JOURNAL Unpublished (2003)
 COMMENT Contact: Nahm B.H.
 Genomics and Bioinformatics, Myongji University of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahn@ggbio.com, bhnahn@bio.myongji.ac.kr.
 FEATURES source
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultivar="MacKdougall"
 /db_xref="taxon:39947"
 /clone="30DGS--04-D07"
 /tissue_type="leaf"
 /dev_stage="30 days after germination"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."
 ORIGIN
 Query Match 72.7%; Score 16; DB 7; Length 342;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 CUCACUCGAGCUCT 21
 Db 324 CTCACCTGGAGCTCT 309
 RESULT 25
 CF299102/C 343 bp mRNA linear EST 15-AUG-2003
 DEFINITION 7LEAF-05-H23.91 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--05-H23, mRNA sequence.
 ACCESSION CF300860
 VERSION EST
 KEYWORDS SOURCE
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bhrhartoidea; Orzyeae; Orzya.
 REFERENCE 1 (bases 1 to 343)
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
 TITLE Large-scale Sequencing Analysis of Rice ESTs
 ORIGIN
 Query Match 72.7%; Score 16; DB 7; Length 340;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 Qy 6 CUCACUCGAGCUCT 21

JOURNAL	UNPUBLISHED (2003)	ORIGIN
UNPUBLISHED (2003)	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@eggbio.com, bhnahm@bio.myongji.ac.kr.	Query Match 72.7%; Best Local Similarity 75.0%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
FEATURES	source 1. .343 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nacidong" /db_xref="taxon:39947" /clone="7LEAF--05-H23" /tissue_type="leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."	RESULT 27 B1810487 LOCUS J009E03 DEFINITION Oryza sativa mature leaf library induced by M.grisea Oryza sativa cDNA clone J009E03, mRNA sequence. ACCESSION B1810487 VERSION B1810487.1 KEYWORDS EST. ORGANISM Oryza sativa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. REFERENCE 1 (bases 1 to 356) AUTHORS Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu, H.F., Jiang, Y.X., Yu, F.C., Gao, Q.Y. and Lou, Y.C. TITLE A Gene Expression Screen in Oryza sativa JOURNAL Unpublished (2001) COMMENT Contact: Haibo Dong, Debao Li Zhejiang University Kaixuan Road 268#, Hangzhou, Zhejiang, P.R. China Tel: 0086-571-86832051 Fax: 0086-571-86961525 Email: webmaster@estarray.org, URL: http://www.estarray.org Seq primer: M13 forward primer. Location/Qualifiers 1. .350 /organism="Oryza sativa" /mol_type="mRNA" /db_xref="taxon:45320" /clone="J009E03" /tissue_type="leaf" /dev_stage="mature stage" /clone_lib="Oryza sativa mature leaf library induced by M.grisea" /note="vector: pSport2"
UNPUBLISHED (2003)	ORIGIN	Query Match 72.7%; Best Local Similarity 75.0%; Matches 12; Conservative 4; Mismatches 0; Gaps 0;
FEATURES	source 1. .343 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nacidong" /db_xref="taxon:39947" /clone="7LEAF--07-L05" /tissue_type="leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."	RESULT 26 CF302308/C LOCUS J009E03 DEFINITION 7LEAF--07-L05_b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa (japonica cultivar-group) cDNA clone 7LEAF--07-L05, mRNA sequence. ACCESSION CF302308 VERSION CF302308.1 KEYWORDS ORYZA sativa (japonica cultivar-group) ORGANISM Oryza sativa (japonica cultivar-group) Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Ehrhartoideae; Oryzeae; Oryza. REFERENCE 1 (bases 1 to 349) AUTHORS Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H. TITLE Large-scale Sequencing Analysis of Rice ESTs JOURNAL Unpublished (2003) COMMENT Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, MyongJi University Yongin, Kyonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@eggbio.com, bhnahm@bio.myongji.ac.kr.
UNPUBLISHED (2003)	ORIGIN	Query Match 72.7%; Best Local Similarity 75.0%; Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
FEATURES	source 1. .349 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nacidong" /db_xref="taxon:39947" /clone="7LEAF--07-L05" /tissue_type="leaf" /dev_stage="7 days after germination" /lab_host="E.coli DH10B" /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)" /note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."	RESULT 28 CF333939/C LOCUS J009E03 DEFINITION 7LEAF--03-A17-91 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone JMT-03-A17, mRNA sequence. ACCESSION CF333939 VERSION CF333939.1 KEYWORDS EST. ORGANISM Oryza sativa (japonica cultivar-group) Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

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Result No.	Score	Query	Match	Length	DB	ID	Description
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C 2	14	63.6	348	3	US-09-134-001C-2127	Sequence 2127, Ap	Sequence 2127, Ap
C 3	14	63.6	428	4	US-09-210-767-8934	Sequence 8934, Ap	Sequence 8934, Ap
C 4	14	63.6	428	4	US-09-270-767-24276	Sequence 24276, A	Sequence 24276, A
C 5	14	63.6	3170	4	US-09-710-779-3849	Sequence 3849, Ap	Sequence 3849, Ap
C 6	14	63.6	4329	4	US-09-710-719-2051	Sequence 2051, Ap	Sequence 2051, Ap
C 7	14	63.6	300598	4	US-09-149-016-11868	Sequence 11868, A	Sequence 11868, A
C 8	14	63.6	302604	4	US-09-949-016-14588	Sequence 14588, A	Sequence 14588, A
C 9	14	63.6	306504	4	US-09-949-016-14589	Sequence 14589, A	Sequence 14589, A
C 10	14	63.6	3083362	4	US-09-949-016-17119	Sequence 17119, A	Sequence 17119, A
C 11	14	63.6	4403765	3	US-09-103-840A-2	Sequence 2, Appl;	Sequence 2, Appl;
C 12	14	63.6	4411529	3	US-09-103-840A-1	Sequence 1, Appl;	Sequence 1, Appl;
C 13	13	59.1	240	4	US-09-88-039A-216	Sequence 216, App	Sequence 216, App
C 14	13	59.1	601	4	US-09-949-016-22714	Sequence 27714, A	Sequence 27714, A
C 15	13	59.1	601	4	US-09-149-016-60781	Sequence 60781, Ap	Sequence 60781, Ap
C 16	13	59.1	601	4	US-09-149-016-60782	Sequence 60782, A	Sequence 60782, A
C 17	13	59.1	601	4	US-09-949-016-60783	Sequence 60783, A	Sequence 60783, A
C 18	13	59.1	601	4	US-09-949-016-60784	Sequence 60784, A	Sequence 60784, A
C 19	13	59.1	601	4	US-09-949-016-164641	Sequence 164641, Ap	Sequence 164641, Ap
C 20	13	59.1	1161	4	US-09-543-681A-3861	Sequence 3861, Ap	Sequence 3861, Ap
C 21	13	59.1	1411	4	US-09-149-016-505	Sequence 4615, Ap	Sequence 4615, Ap
C 22	13	59.1	1546	4	US-09-620-312D-452	Sequence 452, Ap	Sequence 452, Ap
C 23	13	59.1	3250	3	US-09-221-017B-360	Sequence 960, App	Sequence 960, App
C 24	13	59.1	3935	3	US-09-060-182-1	Sequence 1, Appl	Sequence 1, Appl
C 25	13	59.1	4082	4	US-09-949-016-2722	Sequence 2722, Ap	Sequence 2722, Ap
C 26	13	59.1	6015	4	US-09-525-305-50	Sequence 50, App	Sequence 50, App

c 101	12	54.5	832	2	US-08-686 417-1	Sequence 1, Appli	Sequence 1, Appli
c 102	12	54.5	1047	4	US-09-328-3329	Sequence 3329, Ap	Sequence 3, Appli
c 103	12	54.5	1070	3	US-08-904 284-1	Sequence 1, Appli	Sequence 1, Appli
c 104	12	54.5	1236	4	US-09-489 039A 6813	Sequence 6813, Ap	Sequence 1, Appli
c 105	12	54.5	1251	4	US-09-328-352-1546	Sequence 1546, Ap	Sequence 1, Appli
c 106	12	54.5	1260	4	US-09-602-777A-111	Sequence 111, App	Sequence 16, Appli
c 107	12	54.5	1317	4	US-09-543 681A 2202	Sequence 2202, Ap	Sequence 12, Appli
c 108	12	54.5	1330	3	US-09-118-442-29	Sequence 29, App	Sequence 2, Appli
c 109	12	54.5	1330	3	US-09-677-064-29	Sequence 29, Appli	Patent No. 5310678
c 110	12	54.5	1439	2	US-08-495 695B-27	Sequence 27, Appli	Sequence 14, Appli
c 111	12	54.5	1439	5	PCT-US94-14436-27	Sequence 27, Appli	Sequence 35, Appli
c 112	12	54.5	1534	2	US-08-588-983-1	Sequence 1, Appli	Sequence 35, Appli
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c 115	12	54.5	1712	3	US-09-302-620B-105	Sequence 105, App	Sequence 12, Appli
c 116	12	54.5	1712	4	US-09-912-161-45	Sequence 45, Appli	Sequence 12, Appli
c 117	12	54.5	1712	4	US-09-911-781-21	Sequence 23, Appli	Sequence 12, Appli
c 118	12	54.5	1712	4	US-10-400-902-23	Sequence 23, Appli	Sequence 12, Appli
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c 120	12	54.5	1722	4	US-09-949-016-1241	Sequence 3241, Ap	Sequence 12, Appli
c 121	12	54.5	1722	4	US-08-663-566A-10	Sequence 10, Appli	Sequence 12, Appli
c 122	12	54.5	1734	2	US-08-912-161-45	Sequence 10, Appli	Sequence 12, Appli
c 123	12	54.5	1734	2	US-08-288-605A-10	Sequence 10, Appli	Sequence 12, Appli
c 124	12	54.5	1734	2	US-08-362-240A-10	Sequence 10, Appli	Sequence 12, Appli
c 125	12	54.5	1734	3	US-08-804-372A-8	Sequence 8, Appli	Sequence 12, Appli
c 126	12	54.5	1734	5	PCT-US95-01245-10	Sequence 10, Appli	Sequence 2065, Ap
c 127	12	54.5	1759	4	US-09-667-135-3	Sequence 3, Appli	Sequence 12, Appli
c 128	12	54.5	1871	4	US-09-949-016-3156	Sequence 3156, Ap	Sequence 3, Appli
c 129	12	54.5	1871	4	US-09-949-016-3242	Sequence 3242, Ap	Sequence 3, Appli
c 130	12	54.5	1907	1	US-07-820-154A-29	Sequence 29, Appli	Sequence 33, Appli
c 131	12	54.5	1907	2	US-08-097-554A-29	Sequence 29, Appli	Sequence 33, Appli
c 132	12	54.5	1907	3	US-08-480-640A-29	Sequence 29, Appli	Sequence 33, Appli
c 133	12	54.5	1907	3	US-08-295-802-29	Sequence 29, Appli	Sequence 33, Appli
c 134	12	54.5	1907	3	US-09-949-016-3156	Sequence 29, Appli	Sequence 33, Appli
c 135	12	54.5	1907	3	US-08-375-992A-29	Sequence 29, Appli	Sequence 33, Appli
c 136	12	54.5	1907	4	US-08-472-679B-29	Sequence 29, Appli	Sequence 33, Appli
c 137	12	54.5	1907	5	PCT-US93-00324-29	Sequence 29, Appli	Sequence 33, Appli
c 138	12	54.5	2037	3	US-08-913-942-14	Sequence 14, Appli	Sequence 14, Appli
c 139	12	54.5	2037	3	US-08-684-707-14	Sequence 14, Appli	Sequence 14, Appli
c 140	12	54.5	2079	3	US-08-268-347A-29	Sequence 25, Appli	Sequence 14, Appli
c 141	12	54.5	2154	4	US-09-583-110-1968	Sequence 1968, Ap	Sequence 14, Appli
c 142	12	54.5	2166	4	US-09-107-433-216	Sequence 216, App	Sequence 14, Appli
c 143	12	54.5	2307	4	US-09-786-480B-1	Sequence 1, Appli	Sequence 1, Appli
c 144	12	54.5	2417	3	US-09-439-313-334	Sequence 334, App	Sequence 1, Appli
c 145	12	54.5	2417	3	US-09-352-616A-334	Sequence 334, App	Sequence 1, Appli
c 146	12	54.5	2417	3	US-09-232-149A-334	Sequence 334, App	Sequence 1, Appli
c 147	12	54.5	2417	4	US-09-536-215-334	Sequence 334, App	Sequence 1, Appli
c 148	12	54.5	2417	4	US-09-685-166A-334	Sequence 334, App	Sequence 1, Appli
c 149	12	54.5	2417	4	US-09-688-489-334	Sequence 334, App	Sequence 1, Appli
c 150	12	54.5	2417	4	US-09-426-142-334	Sequence 334, App	Sequence 1, Appli
c 151	12	54.5	2417	4	US-09-759-143-334	Sequence 334, App	Sequence 1, Appli
c 152	12	54.5	2417	4	US-09-651-236-334	Sequence 334, App	Sequence 1, Appli
c 153	12	54.5	2433	4	US-08-300-598A-24	Sequence 24, Appli	Sequence 14, Appli
c 154	12	54.5	2437	3	US-08-904-284-25	Sequence 6, Appli	Sequence 14, Appli
c 155	12	54.5	2481	1	US-08-290-301-1	Sequence 1, Appli	Sequence 14, Appli
c 156	12	54.5	2481	3	US-08-013-598-1	Sequence 55, Appli	Sequence 14, Appli
c 157	12	54.5	2484	1	US-07-841-997A-1	Sequence 1, Appli	Sequence 14, Appli
c 158	12	54.5	2718	3	US-09-651-656-14	Sequence 55, Appli	Sequence 14, Appli
c 159	12	54.5	2718	3	US-09-903-012B-55	Sequence 55, Appli	Sequence 14, Appli
c 160	12	54.5	2860	3	US-09-900-797-55	Sequence 87, Appli	Sequence 14, Appli
c 161	12	54.5	2861	3	US-09-221-017B-871	Sequence 55, Appli	Sequence 14, Appli
c 162	12	54.5	2861	4	US-09-398-395A-55	Sequence 55, Appli	Sequence 14, Appli
c 163	12	54.5	2861	4	US-09-895-752-55	Sequence 55, Appli	Sequence 14, Appli
c 164	12	54.5	2861	4	US-09-903-012B-55	Sequence 55, Appli	Sequence 14, Appli
c 165	12	54.5	2861	4	US-09-903-012B-55	Sequence 55, Appli	Sequence 14, Appli
c 166	12	54.5	2968	3	US-09-527-058-6	Sequence 29, Appli	Sequence 14, Appli
c 167	12	54.5	3036	3	US-09-268-347-29	Sequence 23, Appli	Sequence 14, Appli
c 168	12	54.5	3115	3	US-09-221-017B-849	Sequence 84, Appli	Sequence 14, Appli
c 169	12	54.5	3294	3	US-08-409-995-1	Sequence 1, Appli	Sequence 14, Appli
c 170	12	54.5	3294	3	US-08-685-467-1	Sequence 1, Appli	Sequence 14, Appli
c 171	12	54.5	3294	3	US-08-913-942-1	Sequence 1, Appli	Sequence 14, Appli
c 172	12	54.5	3294	3	US-09-268-347-43	Sequence 43, Appli	Sequence 14, Appli
c 173	12	54.5	35707	4	US-09-949-016-17120	Sequence 17120, Ap	Sequence 14, Appli

RESULT 1
 US-09-949-016-16420/c
 Sequence 16420, Application US/09949016
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768

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 54.5 43804 4 US-09-970-711-1
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 54.5 44999 4 US-09-949-016-14832
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 54.5 55703 4 US-09-949-016-17871
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 Sequence 14227, A
 Sequence 17362, A
 Sequence 17490, A
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 Sequence 15402, A
 Sequence 16719, A
 Sequence 13032, A
 Sequence 13807, A
 Sequence 13514, A
 Sequence 15494, A

ALIGNMENTS

RESULT 2
 US-09-134-001C-2127
 Sequence 2127, Application US/09134001C
 ; GENERAL INFORMATION:
 ; APPLICANT: Lynn Doucette-Stamm et al
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 ; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: GTC-007
 ; CURRENT APPLICATION NUMBER: US/09/134-001C
 ; CURRENT FILING DATE: 1998-08-13
 ; PRIOR APPLICATION NUMBER: US 60/064,964
 ; PRIOR FILING DATE: 1997-11-08
 ; PRIOR APPLICATION NUMBER: US 60/055,779
 ; PRIOR FILING DATE: 1997-08-14
 ; NUMBER OF SEQ ID NOS: 5574
 ; SEQ ID NO: 2127
 ; LENGTH: 348
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-054
 ; CURRENT APPLICATION NUMBER: US/09/270-767-8994
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SEQ ID NO: 8994
 ; LENGTH: 428
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-054
 ; CURRENT APPLICATION NUMBER: US/09/270-767-8994
 ; NUMBER OF SEQ ID NOS: 62517
 ; SEQ ID NO: 8994
 ; LENGTH: 428
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-054
 ; CURRENT APPLICATION NUMBER: US/09/270-767-8994
 ; NUMBER OF SEQ ID NOS: 62517
 ; SEQ ID NO: 8994
 ; LENGTH: 428
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-054
 ; CURRENT APPLICATION NUMBER: US/09/270-767-8994
 ; NUMBER OF SEQ ID NOS: 62517
 ; SEQ ID NO: 8994
 ; LENGTH: 428

Query Match 68.2%; Score 15; DB 4;
 Best Local Similarity 80.0%; Pred. No. 5.2;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 CACUCGUGAGCCUCC 22
 Db 140861 CACTCGTAGCTCT 140847

Query Match 68.2%; Score 15; DB 4;
 Best Local Similarity 80.0%; Pred. No. 5.2;
 Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGACUCACUCGU 14
 Db 134 GTCGACTACTCTGT 147

Query Match 63.6%; Score 14; DB 3;
 Best Local Similarity 71.4%; Pred. No. 26;
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 GUGACUCACUCGU 14
 Db 134 GTCGACTACTCTGT 147

RESULT 3
 US-09-270-767-8994
 Sequence 8994, Application US/092707767
 ; GENERAL INFORMATION:
 ; Patent No. 6703491
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-054
 ; CURRENT APPLICATION NUMBER: US/09/270-767-8994
 ; NUMBER OF SEQ ID NOS: 62517
 ; SEQ ID NO: 8994
 ; LENGTH: 428
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768

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Query Match      63.6%;  Score 14;  DB 4;  Length 428;
Best Local Similarity 71.4%;  Pred. No. 26;  Gaps 0;
Matches 10;  Conservative 4;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   7 UCACUCGUGAGCUC 20
Db   356 TCACTCGTAGCTC 369

RESULT 4
US-09-270-767-24276
; Sequence 24276, Application US/092270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; CURRENT APPLICATION NUMBER: US/09-03-17
; FILE REFERENCE: File Reference: 7326-094
; CURRENT FILING DATE: 1999-03-17
; SEQ ID NO: 62217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24276
; LENGTH: 428
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-24276

Query Match      63.6%;  Score 14;  DB 4;  Length 428;
Best Local Similarity 71.4%;  Pred. No. 26;  Gaps 0;
Matches 10;  Conservative 4;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   7 UCACUCGUGAGCUC 20
Db   356 TCACTCGTAGCTC 369

RESULT 5
US-09-710-279-3849
; Sequence 3849, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3849
; LENGTH: 3170
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence

Qy   1 GUGAACUCACUCGU 14
Db   1090 GTGAACTACTCGT 1103

RESULT 6
US-09-710-279-3849
; Sequence 2051, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

Qy   1 GUGAACUCACUCGU 14
Db   1090 GTGAACTACTCGT 1103

RESULT 7
US-09-949-016-11868/c
; Sequence 11868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11868
; LENGTH: 300598
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ..(300598)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11868

Query Match      63.6%;  Score 14;  DB 4;  Length 300598;
Best Local Similarity 78.6%;  Pred. No. 21;
Matches 11;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   9 ACUCUGAGCCU 22
Db   93184 ACTGTTGAGCTCT 93171

RESULT 8
US-09-949-016-14588/c
; Sequence 14588, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

Qy   1 GUGAACUCACUCGU 14
Db   1090 GTGAACTACTCGT 1103

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FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949,016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 20/012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 14588
 LENGTH: 30264
 TYPE: DNA
 ORGANISM: Human
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1) .. (302604)
 OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-14588

Query Match 63.6%; Score 14; DB 4; Length 302604;
 Best Local Similarity 78.6%; Pred. No. 21;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACUGUGAGCTT 22
 Db 143190 ACTCTGAGCTT 143177

RESULT 9
 US-09-949-016-14589/C
 Sequence 14589, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 20/012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 14589
 ; LENGTH: 30264
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1) .. (302604)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-14589

Query Match 63.6%; Score 14; DB 4; Length 302604;
 Best Local Similarity 78.6%; Pred. No. 21;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACUGUGAGCTT 22
 Db 143190 ACTCTGAGCTT 143177

RESULT 10
 US-09-949-016-17119/C
 Sequence 17119, Application US/09949016
 ; Patent No. 612339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 20/012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 17119
 ; LENGTH: 303362
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1) .. (303362)
 ; OTHER INFORMATION: n = A,T,C or G
 US-09-949-016-17119

Query Match 63.6%; Score 14; DB 4; Length 303362;
 Best Local Similarity 78.6%; Pred. No. 21;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ACUCGGAGCTT 22
 Db 143006 ACTCGTGAGCTT 142993

RESULT 11
 US-09-103-840A-2/C
 Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: VENTER, John C.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, Claire M.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; FILE REFERENCE: 243-66-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; NAME/KEY: CDC 1551
 ; LOCATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 US-09-103-840A-2

Query Match 63.6%; Score 14; DB 3; Length 4403765;
 Best Local Similarity 71.4%; Pred. No. 18;
 Matches 10; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 6 CUCACUCGUGACCU 19
 Db 786568 CTCATCTGAGCTT 786555

RESULT 12
 US-09-103-840A-1/C
 Sequence 1, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 20/012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 1

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; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24:66-20007.00
; CURRENT APPLICATION NUMBER: US/09/103, 840A
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
; US-09-103-840A-1

; NUMBER OF SEQ ID NOS: 207012 ; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 27714 ; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-27714

Query Match 59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1.e+02; 3; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 3; File Reference: CLO01307

Qy 4 AACUCACUGUGA 16
Db 238 AACTACCTCGTGA 250

RESULT 15
US-09-949-016-60781/C
; Sequence 60781, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 60781
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-60781

Query Match 59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1.e+02; 3; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 3; File Reference: CLO01307

Qy 1 GUGAACACUGUG 13
Db 601 GTGAACTCACTCG 589

RESULT 16
US-09-949-016-60782/C
; Sequence 60782, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 60782
; LENGTH: 601
; TYPE: DNA

RESULT 17
US-09-949-016-27714
; Sequence 27714, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 60782
; LENGTH: 601
; TYPE: DNA

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; ORGANISM: Human
US-09-949-016-60782

Query Match 59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0;
Gaps 0;
Qy 1 GUGAACUACUCG 13
|:|||:||:||:
Db 339 GTGAACTCACTCG 327

RESULT 17
US-09-949-016-60783/C
; Sequence 60783, Application US/09949016

; GENERAL INFORMATION:
; Patent No. 6812339

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 60783
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60783

Query Match 59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0;
Gaps 0;
Qy 1 GUGAACUACUCG 13
|:|||:||:||:
Db 332 GTGAACTCACTCG 320

RESULT 18
US-09-949-016-60784/C
; Sequence 60784, Application US/09949016

; GENERAL INFORMATION:
; Patent No. 6812339

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 60784
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-60784

Query Match 59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0;
Gaps 0;
Qy 1 GUGAACUACUCG 13
|:|||:||:||:
Db 233 GTGAACTCACTCG 221

RESULT 19
US-09-949-016-164641
; Sequence 164641, Application US/09949016

; GENERAL INFORMATION:
; Patent No. 6812339

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 164641
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-164641

Query Match 59.1%; Score 13; DB 4; Length 601;
Best Local Similarity 76.9%; Pred. No. 1e+02;
Matches 10; Conservative 3; Mismatches 0; Indels 0;
Gaps 0;
Qy 4 AACUGACUGCGA 16
|:|||:||:||:
Db 238 AACUGACUGCGA 250

RESULT 20
US-09-54-681A-3861
; Sequence 3861, Application US/09543681A

; GENERAL INFORMATION:
; Patent No. 6605709

; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A.
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO: 3861
; LENGTH: 1161
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-54-681A-3861

Query Match 59.1%; Score 13; DB 4; Length 1161;
Best Local Similarity 69.2%; Pred. No. 1e+02;
Matches 9; Conservative 4; Mismatches 0; Indels 0;
Gaps 0;
Qy 7 UCACUGUGAGCU 19
|:|||:||:||:
Db 170 TCACUGTCAGCT 182

RESULT 21
US-09-949-016-505
; Sequence 505, Application US/09949016

Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 505
 LENGTH: 1411
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-505

Query Match 59.1%; Score 13; DB 4; Length 1411;
 Best Local Similarity 76.9%; Pred. No. 1e-02;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACUCACUCUGUGA 16
 Db 453 AACTCACTCGTGA 465

RESULT 22
 US-09-949-016-4615
 Sequence 4615, Application US/09949016
 Patent No. 6812339
 GENERAL INFORMATION:
 APPLICANT: VENTER, J. Craig et al.
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CLO01307
 CURRENT APPLICATION NUMBER: US/09/949, 016
 CURRENT FILING DATE: 2000-04-14
 PRIOR APPLICATION NUMBER: 60/241,755
 PRIOR FILING DATE: 2000-10-20
 PRIOR APPLICATION NUMBER: 60/237,768
 PRIOR FILING DATE: 2000-10-03
 PRIOR APPLICATION NUMBER: 60/231,498
 PRIOR FILING DATE: 2000-09-08
 NUMBER OF SEQ ID NOS: 207012
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 4615
 LENGTH: 1411
 TYPE: DNA
 ORGANISM: Human
 US-09-949-016-4615

Query Match 59.1%; Score 13; DB 4; Length 1411;
 Best Local Similarity 76.9%; Pred. No. 1e-02;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACUCACUCUGUGA 16
 Db 453 AACTCACTCGTGA 465

RESULT 23
 US-09-620-312D-452
 Sequence 452, Application US/09620312D
 Patent No. 6569652
 GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Liu, Chenghua
 APPLICANT: Asundi, Vinod

APPLICANT: Zhang, Jie
 APPLICANT: Ren, Feiyan
 APPLICANT: Chen, Rui-hong
 APPLICANT: Zhao, Qing A.
 APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yunging
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: John Tillinghast
 APPLICANT: Drmanac, Radivoje T.
 TITLE OF INVENTION: No. 6569662el Nucleic Acids and
 TITLE OF INVENTION: No. 6569662el Nucleic Acids and
 FILE REFERENCE: 78CIP2B
 CURRENT APPLICATION NUMBER: US/09/620,312D
 CURRENT FILING DATE: 2000-07-19
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1105
 SOFTWARE: pt_PL_genes Version 1.0
 SEQ ID NO: 452
 LENGTH: 1546
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (404) .. (1189)
 US-09-620-312D-452

Query Match 59.1%; Score 13; DB 4; Length 1546;
 Best Local Similarity 76.9%; Prd. No. 99;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AACUCACUCUGUGA 16
 Db 572 AACTCACTCGTGA 584

RESULT 24
 US-09-221-017B-960/c
 Sequence 960, Application US/09221017B
 Patent No. 6444799
 GENERAL INFORMATION:
 APPLICANT: Ross, Bruce C.
 TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
 NUMBER OF SEQUENCES: 1120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 755 PAGE MILL ROAD
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION NUMBER: US/09/221,017B
 FILING DATE: 23-DEC-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: P1182
 FILING DATE: 31-DEC-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: P1546
 FILING DATE: 30-JAN-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PP2911
 FILING DATE: 09-APR-1998

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/AU98/01023
 FILING DATE: 10-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Monroy, Gladys H
 REGISTRATION NUMBER: 32,430
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-813-5600
 TELEX: 650-494-0792

INFORMATION FOR SEQ ID NO: 960:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3250 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: UNKNOWN
 ORIGINAL SOURCE:
 ORGANISM: PORYPHYROMONAS GINGIVALIS
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1...3250
 US-09-221-017B-960

Query Match 59.1%; Score 13; DB 3; Length 3250;
 Best Local Similarity 76.9%; Pred. No. 97;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCHACUCG 13
 Db 2826 GTGAACTCTACTCG 2814

RESULT 25
 US-09-060-482-1/C
 ; Sequence 1, Application US/09060482
 ; GENERAL INFORMATION:
 ; APPLICANT: Layne, Matthew D.
 ; ATTORNEY: Yet, Shaw-Fang
 ; TITLE OF INVENTION: AORTIC CARDOXYPEPTIDASE-LIKE POLYPEPTIDE
 ; FILE REFERENCE: 0543/036001
 ; CURRENT APPLICATION NUMBER: US/09/060,482
 ; CURRENT FILING DATE: 1998-04-15
 ; EARLIER FILING DATE: 1997-03-14
 ; EARLIER APPLICATION NUMBER: US 60\013,439
 ; EARLIER FILING DATE: 1996-03-15
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 3935
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (140)...(3613)

Query Match 59.1%; Score 13; DB 3; Length 3935;
 Best Local Similarity 76.9%; Pred. No. 96;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CUCGGAGGAGCTT 22
 Db 1925 CTCGTTGAGCTCT 1913

RESULT 26
 US-09-949-016-2722/C
 ; Sequence 2722, Application US/09949016
 ; Patent No. 681239
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL0013.07
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2722
 ; LENGTH: 4082
 ; TYPE: DNA
 ; ORGANISM: Human
 ; SEQ ID NO 960-2722

Query Match 59.1%; Score 13; DB 4; Length 4082;
 Best Local Similarity 76.9%; Pred. No. 96;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CUCGGAGGAGCTT 22
 Db 2092 CTCGTTGAGCTCT 2080

RESULT 27
 US-09-525-305-50
 ; Sequence 50, Application US/09525305
 ; Patent No. 6806062
 ; GENERAL INFORMATION:
 ; APPLICANT: Hjort, Carsten
 ; ATTORNEY: Hondeel, C.A.M.J.J. van den
 ; APPLICANT: Punt, P.J.
 ; APPLICANT: Shuren, F.H.J.
 ; APPLICANT: Christensen, Tove
 ; TITLE OF INVENTION: Fungal Transcriptional Activator Useful In Methods For Producing
 ; TITLE OF INVENTION: Polypeptides
 ; FILE REFERENCE: 5555,400-US
 ; CURRENT APPLICATION NUMBER: US/09/525,305
 ; CURRENT FILING DATE: 2000-03-14
 ; NUMBER OF SEQ ID NOS: 54
 ; SEQ ID NO 50
 ; LENGTH: 6015
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: pdv8 plasmid

Query Match 59.1%; Score 13; DB 4; Length 6015;
 Best Local Similarity 76.9%; Pred. No. 95;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 10 ACUCUGAGGAGCTT 21
 Db 350 ACTCTGAGCTCT 362

RESULT 28
 US-09-949-016-12281
 ; Sequence 12281, Application US/09949016

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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 12247
; LENGTH: 12247
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12247

Query Match      59.1%;  Score 13;  DB 4;  Length 6831;
Best Local Similarity 69.2%;  Pred. No. 95;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      7 UCACUCUGGAGCU 19
Db      1201 TCACTCGGAGCT 1213

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Job time : 147 secs

RESULT 29
; US-09-949-016-14464/C
; Sequence 14464, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 14464
; LENGTH: 14205
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-14464

Query Match      59.1%;  Score 13;  DB 4;  Length 14205;
Best Local Similarity 76.9%;  Pred. No. 92;  Mismatches 0;  Indels 0;  Gaps 0;
Matches 10;  Conservative 3;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      10 CUCUGGAGCTCTT 22
Db      9218 CTCCTGAGCTCTT 9206

RESULT 30
; US-09-949-016-12247
; Sequence 12247, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 12247
; LENGTH: 14247
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-12247

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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16: /cgn2_6_ptodata/2_pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6_ptodata/2_pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6_ptodata/2_pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6_ptodata/2_pubpna/US10G_PUBCOMB.seq:*
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23: /cgn2_6_ptodata/2_pubpna/US11B_PUBCOMB.seq:*
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25: /cgn2_6_ptodata/2_pubpna/US11D_PUBCOMB.seq:*
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SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
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2	20	90.9	20	21 US-10-831-901A-29740	Sequence 2, Appli
3	20	90.9	525	22 US-10-755-415-166	Sequence 3, Appli
4	20	90.9	1215	21 US-10-831-901A-29766	Sequence 4, Appli
5	20	90.9	1705	21 US-10-699-936-4	Sequence 5, Appli
6	20	90.9	1706	21 US-10-699-936-14	Sequence 6, Appli
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247	13	59.1	747	20	US-10-425-115-141170	Sequence 141170,	200	13	59.1	1787	15
248	13	59.1	796	9	US-09-770-445-832	Sequence 832, App	200	13	59.1	1788	15
249	13	59.1	797	19	US-10-437-663-47033	Sequence 47033, A	200	13	59.1	1789	15
250	13	59.1	804	20	US-10-425-115-11740	Sequence 11740, A	200	13	59.1	1790	15
251	13	59.1	816	9	US-09-815-242-7363	Sequence 7363, Ap	200	13	59.1	1791	15
252	13	59.1	816	19	US-09-815-242-7527	Sequence 7527, Ap	200	13	59.1	1792	15
253	13	59.1	816	17	US-10-282-122A-22850	Sequence 22850, A	200	13	59.1	1793	15
254	13	59.1	816	18	US-10-335-977-120	Sequence 120, App	200	13	59.1	1794	15
255	13	59.1	816	18	US-10-335-977-121	Sequence 121, App	200	13	59.1	1795	15
256	13	59.1	820	20	US-10-425-115-14034	Sequence 14034, A	200	13	59.1	1796	15
257	13	59.1	820	20	US-10-279-579A-3	Sequence 3, Appli	200	13	59.1	1797	15
258	13	59.1	840	18	US-10-335-977-122	Sequence 122, App	200	13	59.1	1798	15
259	13	59.1	855	20	US-10-315-93-30292	Sequence 30292, A	200	13	59.1	1799	15
260	13	59.1	877	20	US-10-425-115-12436	Sequence 12436, A	200	13	59.1	1800	15
261	13	59.1	885	9	US-09-925-301-14	Sequence 14, Appli	200	13	59.1	1801	15
262	13	59.1	901	20	US-10-425-115-14035	Sequence 14035, A	200	13	59.1	1802	15
263	13	59.1	901	20	US-10-027-632-120838	Sequence 120838, A	200	13	59.1	1803	15
264	13	59.1	943	13	US-10-027-632-120839	Sequence 120839,	200	13	59.1	1804	15
265	13	59.1	943	13	US-10-027-632-120840	Sequence 120840,	200	13	59.1	1805	15
266	13	59.1	943	17	US-10-027-632-120838	Sequence 120838,	200	13	59.1	1806	15
267	13	59.1	943	17	US-10-027-632-120839	Sequence 120839,	200	13	59.1	1807	15
268	13	59.1	943	17	US-10-425-115-14040	Sequence 14040, App	200	13	59.1	1808	15
269	13	59.1	944	10	US-09-934-455-7	Sequence 7, Appli	200	13	59.1	1809	15
270	13	59.1	947	14	US-10-286-564-33	Sequence 33, Appli	200	13	59.1	1810	15
271	13	59.1	947	14	US-10-225-066A-227	Sequence 327, App	200	13	59.1	1811	15
272	13	59.1	947	17	US-10-374-580A-13	Sequence 13, Appli	200	13	59.1	1812	15
273	13	59.1	947	18	US-10-412-599B-67	Sequence 67, Appli	200	13	59.1	1813	15
274	13	59.1	954	10	US-09-738-626-532	Sequence 532, App	200	13	59.1	1814	15
275	13	59.1	954	10	US-10-767-701-13098	Sequence 13098, A	200	13	59.1	1815	15
276	13	59.1	1137	17	US-10-369-493-27586	Sequence 27586, A	200	13	59.1	1816	15
277	13	59.1	1146	17	US-10-38-492-12465	Sequence 12465, A	200	13	59.1	1817	15
278	13	59.1	1177	18	US-10-425-114-28069	Sequence 28069, A	200	13	59.1	1818	15
279	13	59.1	1387	17	US-10-225-066A-557	Sequence 657, App	200	13	59.1	1819	15
280	13	59.1	1387	17	US-10-74-780A-315	Sequence 315, App	200	13	59.1	1820	15
281	13	59.1	1411	9	US-09-380-107-38215	Sequence 3821, Ap	200	13	59.1	1821	15
282	13	59.1	1414	18	US-10-425-114-28742	Sequence 28742, A	200	13	59.1	1822	15
283	13	59.1	1423	17	US-10-425-114-27173	Sequence 27173, A	200	13	59.1	1823	15
284	13	59.1	1514	18	US-10-424-599-45112	Sequence 45112, A	200	13	59.1	1824	15
285	13	59.1	1546	15	US-10-037-720-452	Sequence 452, App	200	13	59.1	1825	15
286	13	59.1	1546	17	US-10-117-724-452	Sequence 452, App	200	13	59.1	1826	15
287	13	59.1	1556	9	US-09-764-881-47	Sequence 47, Appli	200	13	59.1	1827	15
288	13	59.1	1556	10	US-09-764-881-47	Sequence 47, Appli	200	13	59.1	1828	15
289	13	59.1	1556	11	US-09-764-875-537	Sequence 537, Appli	200	13	59.1	1829	15
290	13	59.1	1556	11	US-10-242-115-49236	Sequence 49236, A	200	13	59.1	1830	15
291	13	59.1	1556	17	US-10-158-057-154	Sequence 154, App	200	13	59.1	1831	15
292	13	59.1	1581	17	US-10-39-930-4802	Sequence 4802, Ap	200	13	59.1	1832	15
293	13	59.1	1642	18	US-10-425-114-5598	Sequence 5598, Ap	200	13	59.1	1833	15
294	13	59.1	1642	20	US-10-425-115-49236	Sequence 49236, A	200	13	59.1	1834	15
295	13	59.1	1695	20	US-10-425-115-116401	Sequence 116401, A	200	13	59.1	1835	15
296	13	59.1	1724	18	US-10-425-114-35588	Sequence 35588, A	200	13	59.1	1836	15
297	13	59.1	1739	17	US-10-374-780A-972	Sequence 972, App	200	13	59.1	1837	15
298	13	59.1	1743	18	US-10-425-114-1957	Sequence 1957, Ap	200	13	59.1	1838	15
299	13	59.1	1748	18	US-10-425-114-7773	Sequence 7773, Ap	200	13	59.1	1839	15

RESULT 3
 US-10-755-415-166
 Sequence 166, Application US/10755415
 Publication No. US2005013480A1
 GENERAL INFORMATION:
 ; APPLICANT: BRAHMACHARI, SAMIR KUMAR
 ; APPLICANT: DASH, DEBASIS
 ; APPLICANT: SHARMA, RAMAKANT
 ; APPLICANT: MAHESHWARI, JITENDRA KUMAR
 TITLE OF INVENTION: A COMPUTER BASED VERSATILE METHOD FOR IDENTIFYING PROTEIN CODING
 FILE REFERENCE: 026533-00029
 CURRENT APPLICATION NUMBER: US/10/755,415
 CURRENT FILING DATE: 2004-01-13
 PRIORITY APPLICATION NUMBER: 10/727,989
 PRIORITY FILING DATE: 2003-12-05
 NUMBER OF SEQ ID NOS: 373
 SOFTWARE: Patentin version 3.3
 SEQ ID NO 166
 LENGTH: 925
 TYPE: DNA
 ORGANISM: Sars coronavirus
 US-10-755-415-166

Query Match 90.9%; Score 20; DB 21; Length 20;
 Best Local Similarity 75.0%; Pred. No. 0.02; Mismatches 5; Indels 0; Gaps 0;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCGGAGCUC 20
 Db 20 GTGAACTCACTCGTGAAGCTC 1

RESULT 4
 US-10-831-901A-29766
 Sequence 29766, Application US/10831901A
 Publication No. US20050100885A1
 GENERAL INFORMATION:
 ; APPLICANT: Crooke, Stanley T.
 ; APPLICANT: Ecker, David J.
 ; APPLICANT: Sampath, Rangarajan
 ; APPLICANT: Freier, Susan M.
 ; APPLICANT: Massire, Christian
 ; APPLICANT: Hoistadler, Steven A.
 ; APPLICANT: Lowery, Kristin Sannes
 ; APPLICANT: Swazye, Eric
 ; APPLICANT: Baker, Brenda F.
 ; APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
 Acute Respiratory Syndrome (SARS)
 ; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
 ; FILE REFERENCE: IIS0083-100 (BIO00080S)
 ; CURRENT APPLICATION NUMBER: US/10/831,901A
 ; CURRENT FILING DATE: 2004-04-26
 ; PRIOR APPLICATION NUMBER: 60/466,426
 ; PRIOR FILING DATE: 2003-04-28
 ; PRIOR APPLICATION NUMBER: 60/468,562
 ; PRIOR FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: 60/467,770
 ; PRIOR FILING DATE: 2003-04-30
 ; PRIOR APPLICATION NUMBER: 60/468,627
 ; PRIOR FILING DATE: 2003-05-06
 ; PRIOR APPLICATION NUMBER: 60/477,637
 ; PRIOR FILING DATE: 2003-06-10
 ; PRIOR APPLICATION NUMBER: 60/483,579
 ; PRIOR FILING DATE: 2003-06-27
 ; NUMBER OF SEQ ID NOS: 30063
 ; SOFTWARE: FastSE Sequence Editor Version 4.0
 SEQ ID NO 780
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Antisense compound
 US-10-831-901A-780

Query Match 90.9%; Score 20; DB 21; Length 20;
 Best Local Similarity 75.0%; Pred. No. 0.013; Mismatches 5; Indels 0; Gaps 0;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCGGAGCUC 20
 Db 20 GTGAACTCACTCGTGAAGCTC 779

RESULT 5
 US-10-599-936-4
 Sequence 4, Application US/10699936
 Publication No. US2005009582A1
 GENERAL INFORMATION:
 ; APPLICANT: Gilliam-Ross, Laura
 ; APPLICANT: Taylor, Jill
 ; APPLICANT: Schilloli, David R.
 ; APPLICANT: Wentworth, David E.
 ; APPLICANT: Jollieck, Joseph D.
 ; TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
 Syndrome Coronavirus
 ; FILE REFERENCE: DHL-07986
 ; CURRENT APPLICATION NUMBER: US/10/699,936
 ; CURRENT FILING DATE: 2003-11-03
 ; NUMBER OF SEQ ID NOS: 87
 ; SOFTWARE: Patentin version 3.2
 ; SEQ ID NO 4
 ; LENGTH: 1706
 ; TYPE: DNA
 ; ORGANISM: SARS-CoV Shanghai LY
 US-10-599-936-4

Query Match 90.9%; Score 20; DB 21; Length 1706;
 Best Local Similarity 75.0%; Pred. No. 0.012; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUCGGAGCUC 20
 Db 697 GTGAACTCACTCGTGAAGCTC 716

RESULT 6
 US-10-699-936-14
 Sequence 14, Application US/10699936
 Publication No. US2005009582A1
 GENERAL INFORMATION:
 ; APPLICANT: Gilliam-Ross, Laura
 ; APPLICANT: Taylor, Jill

APPLICANT: Scholl, David R.
 APPLICANT: Wentworth, David E.
 APPLICANT: Jollie, Joseph D.
 TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory Syndrome Coronavirus
 FILE REFERENCE: DHI-07986
 CURRENT APPLICATION NUMBER: US/10/699,936
 CURRENT FILING DATE: 2003-11-03
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: Patentin, version 3.2
 SEQ ID NO 14
 LENGTH: 1706
 TYPE: DNA
 ORGANISM: SARS coronavirus Shanghai LY
 US-10-699-936-14

Query Match 90.9%; Score 20; DB 21; Length 1706;
 Best Local Similarity 75.0%; Pred. No. 0.012; Mismatches 5; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Number of SEQ ID NOS: 30063

Qy 1 GUGAACUCACUGUGAGCU 20
 Db 697 GTGAACTACTCGTGTGCTC 716

RESULT 7
 FILE REFERENCE: RTI-0689-447-3
 CURRENT APPLICATION NUMBER: US/10/889,447
 CURRENT FILING DATE: 2004-07-12
 PRIORITY FILING DATE: 2003-07-12
 NUMBER OF SEQ ID NOS: 141
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 24774
 TYPE: DNA
 ORGANISM: SARS coronavirus isolate BJ01

FEATURE:
 NAME/KEY: misc_feature
 LOCATION:
 / FILE REFERENCE: ISIS0083-100 (BIOL0008US)
 / CURRENT APPLICATION NUMBER: US/10/831,901A
 / CURRENT FILING DATE: 2004-04-26
 / PRIOR APPLICATION NUMBER: 60/466,426
 / PRIOR FILING DATE: 2003-04-28
 / PRIOR APPLICATION NUMBER: 60/468,562
 / PRIOR FILING DATE: 2003-05-06
 / PRIOR APPLICATION NUMBER: 60/467,770
 / PRIOR FILING DATE: 2003-04-30
 / PRIOR APPLICATION NUMBER: 60/468,627
 / PRIOR FILING DATE: 2003-05-06
 / PRIOR APPLICATION NUMBER: 60/477,637
 / PRIOR FILING DATE: 2003-06-10
 / PRIOR APPLICATION NUMBER: 60/483,579
 / PRIOR FILING DATE: 2003-06-27
 / SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 29748
 LENGTH: 24774
 TYPE: DNA
 ORGANISM: SARS Coronavirus
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 960-959, 2089-2188, 2478-2577, 2877-2976, 3576-3675, 3865-3964,
 / LOCATION: 4134-4233, 5781-5879, 7438-7537, 7837-7936,
 / LOCATION: 8616-8715, 12025-12124, 13984-14003, 16463-16562, 16922-17031,
 / LOCATION: 1738-17480, 18090-18189, 19019-19118, 19478-19577, 20357-20456,
 / LOCATION: 21088-21185, 21945-22044, 23174-23273, 23531
 / OTHER INFORMATION: n = A,T,C or G
 US-10-831-901A-29748

Query Match 90.9%; Score 20; DB 21; Length 24774;
 Best Local Similarity 75.0%; Pred. No. 0.009; Mismatches 5; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Number of SEQ ID NOS: 298

Qy 1 GUGACUCACUGUGAGCU 20
 Db 706 GTGAACTACTCGTGTGCTC 725

RESULT 9
 FILE REFERENCE: RTI-0689-101-3
 CURRENT APPLICATION NUMBER: US/10/889,101
 CURRENT FILING DATE: 2004-07-12
 PRIORITY FILING DATE: 2003-07-12
 NUMBER OF SEQ ID NOS: 141
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 24774
 TYPE: DNA
 ORGANISM: SARS Coronavirus isolate BJ01

FEATURE:
 NAME/KEY: misc_feature
 LOCATION:
 / OTHER INFORMATION: n is any nucleotide
 US-10-889-447-3

Query Match 90.9%; Score 20; DB 21; Length 24774;
 Best Local Similarity 75.0%; Pred. No. 0.009; Mismatches 5; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Number of SEQ ID NOS: 298

Qy 1 GUGAACUCACUGUGAGCU 20
 Db 706 GTGAACTACTCGTGTGCTC 725

RESULT 8
 FILE REFERENCE: RTI-0689-101-3
 CURRENT APPLICATION NUMBER: US/10/889,101
 CURRENT FILING DATE: 2004-07-12
 PRIORITY FILING DATE: 2003-07-12
 NUMBER OF SEQ ID NOS: 298
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 24774
 TYPE: DNA
 ORGANISM: SARS Coronavirus isolate BJ01

FEATURE:
 NAME/KEY: misc_feature
 LOCATION:
 / OTHER INFORMATION: n = A,T,C or G
 US-10-889-101-3

Query Match 90.9%; Score 20; DB 21; Length 24774;
 Best Local Similarity 75.0%; Pred. No. 0.009; Mismatches 5; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Number of SEQ ID NOS: 298

ORGANISM: SARS Coronavirus isolate BJ03
 FEATURE: misc_feature
 LOCATION: n = A,T,C or G
 OTHER INFORMATION: US-10-889-101-5

Query Match 90.9%; Score 20; DB 21; Length 28920;
 Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 5; Gaps 0;
 SEQ ID NO: 776 GUGAACUCACUCUGAGCUC 20
 DB 776 GTGAACTCACTCGTGTAGTC 795

RESULT 14
 US-10-889-101-6
 Sequence 6, Application US/10889101
 Publication No. US20050107324A1
 GENERAL INFORMATION:
 APPLICANT: Bennett, C. Frank
 APPLICANT: Doble, Kenneth W.
 APPLICANT: Jain, Ravi
 TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
 FILE REFERENCE: ISIS0101-100 (RTS-0655US)
 CURRENT APPLICATION NUMBER: US/10/889,101
 CURRENT FILING DATE: 2004-07-12
 PRIOR APPLICATION NUMBER: 60/486,652
 PRIOR FILING DATE: 2003-07-12
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 28920
 TYPE: DNA
 ORGANISM: SARS Coronavirus isolate BJ04
 FEATURE: misc_feature
 LOCATION:
 OTHER INFORMATION: n = A,T,C or G
 US-10-889-101-6

Query Match 90.9%; Score 20; DB 21; Length 28920;
 Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 5; Gaps 0;
 SEQ ID NO: 776 GUGAACUCACUCUGAGCUC 20
 DB 776 GTGAACTCACTCGTGTAGTC 795

RESULT 15
 US-10-831-901A-29819
 Sequence 29819, Application US/10831901A
 Publication No. US20050100885A1
 GENERAL INFORMATION:
 APPLICANT: Crooke, Stanley T.
 APPLICANT: Ecker, David J.
 APPLICANT: Sampath, Rangarajan
 APPLICANT: Freier, Susan M.
 APPLICANT: Massire, Christian
 APPLICANT: Hofstadler, Steven A.
 APPLICANT: Lowery, Kristin Sannes
 APPLICANT: Swazye, Eric
 APPLICANT: Baker, Brenda F.
 APPLICANT: Bennett, C. Frank
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
 Acute Respiratory Syndrome (SARS)
 FILE REFERENCE: ISIS0083-100 (BIO008US)
 CURRENT APPLICATION NUMBER: US/10/831,901A
 CURRENT FILING DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: 60/468,562
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/467,770
 PRIOR FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: 60/468,627
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/477,637
 PRIOR FILING DATE: 2003-06-10
 PRIOR APPLICATION NUMBER: 60/483,579
 PRIOR FILING DATE: 2003-06-27
 NUMBER OF SEQ ID NOS: 30063
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 29742
 LENGTH: 29206
 TYPE: DNA
 ORGANISM: SARS Coronavirus
 US-10-831-901A-29742

Query Match 90.9%; Score 20; DB 21; Length 29206;
 Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 776 GUGAACUCACUCUGAGCUC 20
 DB 776 GTGAACTCACTCGTGTAGTC 795

RESULT 16
 US-10-831-901A-29742
 Sequence 29742, Application US/10831901A
 Publication No. US20050100885A1
 GENERAL INFORMATION:
 APPLICANT: Crooke, Stanley T.
 APPLICANT: Ecker, David J.
 APPLICANT: Sampath, Rangarajan
 APPLICANT: Freier, Susan M.
 APPLICANT: Massire, Christian
 APPLICANT: Hofstadler, Steven A.
 APPLICANT: Lowery, Kristin Sannes
 APPLICANT: Swazye, Eric
 APPLICANT: Baker, Brenda F.
 APPLICANT: Bennett, C. Frank
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
 Acute Respiratory Syndrome (SARS)
 FILE REFERENCE: ISIS0083-100 (BIO008US)
 CURRENT APPLICATION NUMBER: US/10/831,901A
 CURRENT FILING DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: 60/468,562
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/467,770
 PRIOR FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: 60/468,627
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/477,637
 PRIOR FILING DATE: 2003-06-10
 PRIOR APPLICATION NUMBER: 60/483,579
 PRIOR FILING DATE: 2003-06-27
 NUMBER OF SEQ ID NOS: 30063
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 29742
 LENGTH: 29206
 TYPE: DNA
 ORGANISM: SARS Coronavirus
 US-10-831-901A-29742

Query Match 90.9%; Score 20; DB 21; Length 29206;
 Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 776 GUGAACUCACUCUGAGCUC 20
 DB 776 GTGAACTCACTCGTGTAGTC 795

RESULT 17
 US-10-831-901A-29819
 Sequence 29819, Application US/10831901A
 Publication No. US20050100885A1
 GENERAL INFORMATION:
 APPLICANT: Crooke, Stanley T.
 APPLICANT: Ecker, David J.
 APPLICANT: Sampath, Rangarajan
 APPLICANT: Freier, Susan M.
 APPLICANT: Massire, Christian
 APPLICANT: Hofstadler, Steven A.
 APPLICANT: Lowery, Kristin Sannes
 APPLICANT: Swazye, Eric
 APPLICANT: Baker, Brenda F.
 APPLICANT: Bennett, C. Frank
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
 Acute Respiratory Syndrome (SARS)
 FILE REFERENCE: ISIS0083-100 (BIO008US)
 CURRENT APPLICATION NUMBER: US/10/831,901A
 CURRENT FILING DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: 60/468,562
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/467,770
 PRIOR FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: 60/468,627
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/477,637
 PRIOR FILING DATE: 2003-06-10
 PRIOR APPLICATION NUMBER: 60/483,579
 PRIOR FILING DATE: 2003-06-27
 NUMBER OF SEQ ID NOS: 30063
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 29742
 LENGTH: 29206
 TYPE: DNA
 ORGANISM: SARS Coronavirus
 US-10-831-901A-29742

Query Match 90.9%; Score 20; DB 21; Length 29206;
 Best Local Similarity 75.0%; Pred. No. 0.0089; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO: 776 GUGAACUCACUCUGAGCUC 20
 DB 776 GTGAACTCACTCGTGTAGTC 795

```

Db 751 GTGAACTCACTCGTGAGCTC 770
;
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6112_10070_10169, 10560, 10775, 10849_10948, 21378_21477, 22501,
; LOCATION: 23795_23894, 25144_25243, 26737, 26823_26922, 28128, 28463
; OTHER INFORMATION: n = A,T,C or G
; SEQ ID NO: 901A-29738

RESULT 17
Sequence 4, Application US/10889447
Publication No. US2005005307A1
GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Revi
; TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
; FILE REFERENCE: RTS-0685US
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,670
; PRIOR FILING DATE: 2003-07-12
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 29291
; TYPE: DNA
; ORGANISM: SARS coronavirus isolate BJ02
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-4
Query Match 90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GUGAACUCACUGUGAGUC 20
Db 726 GTGAACTCACTCGTGAGCTC 745

RESULT 18
Sequence 29738, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Becker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Horstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swaye, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: IIS0083-100 (B1010008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NO: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 29738
; LENGTH: 29291

RESULT 19
US-10-889-101-4
Sequence 4, Application US/10889101
Publication No. US2005010732A1
GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
; FILE REFERENCE: IIS0101-100 (RTS-065US)
; CURRENT APPLICATION NUMBER: US/10/889,101
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,652
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID: NOS: 298
; SOFTWARE: FastSEQ for Windows Version 4.0
; LENGTH: 29291
; SEQ ID NO: 4
; TYPE: DNA
; ORGANISM: SARS Coronavirus isolate BJ02
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: n = A,T,C or G
US-10-889-101-4
Query Match 90.9%; Score 20; DB 21; Length 29291;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GUGAACUCACUGUGAGUC 20
Db 726 GTGAACTCACTCGTGAGCTC 745

RESULT 20
US-10-901A-29739
Sequence 29739, Application US/10831901A
Publication No. US20050100885A1
GENERAL INFORMATION:
; APPLICANT: Cooke, Stanley T.
; APPLICANT: Becker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadler, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swaye, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: IIS0083-100 (B1010008US)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NO: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 29738
; LENGTH: 29291

```

PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: 60/468,562
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/467,770
 PRIOR FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: 60/468,627
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/477,637
 PRIOR FILING DATE: 2003-05-10
 PRIOR APPLICATION NUMBER: 60/483,579
 PRIOR FILING DATE: 2003-06-27
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 29739
 LENGTH: 29429
 TYPE: DNA
 ORGANISM: SARS Coronavirus
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 960-559, 2509-2608, 3338-3437, 5551, 5767-5866, 7296-7395, 8908,
 LOCATION: 10914-11014, 11744-11843, 14933-15092, 20606, 2053, 21432-21531,
 LOCATION: 25728, 25746, 26631-26730, 28364
 OTHER INFORMATION: n = A,T,C or G
 US-10-831-901A-29739

Query Match 90.9%; Score 20; DB 21; Length 29429;
 Best Local Similarity 75.0%; Pred. No. 0.0089;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUGAGGUC 20
 Db 793 GTGAACTACTCGTGTGCTC 812

RESULT 21
 US-10-889-447-7
 Sequence 7, Application US/10889447
 Publication No. US20050075307A1

GENERAL INFORMATION:
 APPLICANT: Bennett, C. Frank
 APPLICANT: Jain, Ravi
 TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
 FILE REFERENCE: RTS-0685US
 CURRENT APPLICATION NUMBER: US/10/889,447
 CURRENT FILING DATE: 2004-07-12
 PRIOR APPLICATION NUMBER: 60/486,670
 PRIOR FILING DATE: 2003-07-12
 NUMBER OF SEQ ID NOS: 241
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 7
 LENGTH: 29430
 TYPE: DNA
 ORGANISM: SARS coronavirus isolate GZ01
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION:
 OTHER INFORMATION: n is any nucleotide

US-10-889-447-7

Query Match 90.9%; Score 20; DB 21; Length 29430;
 Best Local Similarity 75.0%; Pred. No. 0.0089;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUGAGGUC 20
 Db 760 GTGAACTACTCGTGTGCTC 779

RESULT 22
 US-10-831-901A-29741
 Sequence 29741, Application US/10831901A
 Publication No. US20050100885A1

GENERAL INFORMATION:
 APPLICANT: Cooke, Stanley T.
 APPLICANT: Ecker, David J.
 APPLICANT: Sampath, Rangarajan
 APPLICANT: Freier, Susan M.
 APPLICANT: Massire, Christian
 APPLICANT: Hofstadler, Steven A.
 APPLICANT: Lowery, Kristin Sannes
 APPLICANT: Swayze, Eric
 APPLICANT: Baker, Brenda F.
 APPLICANT: Bennett, C. Frank
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe Acute Respiratory Syndrome (SARS)
 FILE REFERENCE: ISIS0083-100 (B10100080US)
 CURRENT APPLICATION NUMBER: US/10/831,901A
 LENGTH: 29430
 PRIORITY DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: 60/468,562
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/467,770
 PRIOR FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: 60/468,627
 PRIOR FILING DATE: 2003-05-06
 PRIOR APPLICATION NUMBER: 60/477,637
 PRIOR FILING DATE: 2003-06-10
 PRIOR APPLICATION NUMBER: 60/483,579
 PRIOR FILING DATE: 2003-06-27
 NUMBER OF SEQ ID NOS: 30063
 SOFTWARE: FastSEQ For Windows Version 4.0
 SEQ ID NO: 29741
 LENGTH: 29430
 TYPE: DNA
 ORGANISM: SARS Coronavirus
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 6464-6563, 11343-11442, 22557-226666
 OTHER INFORMATION: n = A,T,C or G
 US-10-831-901A-29741

Query Match 90.9%; Score 20; DB 21; Length 29430;
 Best Local Similarity 75.0%; Pred. No. 0.0089;
 Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUGAGGUC 20
 Db 760 GTGAACTACTCGTGTGCTC 779

RESULT 23
 US-10-889-101-7
 Sequence 7, Application US/10889101
 Publication No. US20050107324A1

GENERAL INFORMATION:
 APPLICANT: Bennett, C. Frank
 APPLICANT: Dobie, Kenneth W.
 APPLICANT: Jain, Ravi
 TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
 FILE REFERENCE: ISIS0101-100 (RTS-0655US)
 CURRENT APPLICATION NUMBER: US/10/889,101
 LENGTH: 29430
 PRIORITY DATE: 2004-07-12
 PRIOR APPLICATION NUMBER: 60/486,652
 PRIOR FILING DATE: 2003-07-12
 NUMBER OF SEQ ID NOS: 298
 SOFTWARE: FastSEQ For Windows Version 4.0
 SEQ ID NO: 7
 LENGTH: 29430
 TYPE: DNA
 ORGANISM: SARS Coronavirus isolate GZ01
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION:
 OTHER INFORMATION: n = A,T,C or G

RESULT 22
 US-10-831-901A-29741
 Sequence 29741, Application US/10831901A
 Publication No. US20050100885A1

US-10-889-101-7

Query Match 90.9%; Score 20; DB 21; Length 29430;
Best Local Similarity 75.0%; Pred. No. 0.0089; 0; Gaps 0;
Matches 15; Conservative 5; Mismatches 0; Indels 0;

Qy 1 GUGAACUCACUCCUGAGGCU 20
Db 760 GTGAACTCTCTGGAGTC 779

RESULT 24

US-10-831-901A-29802

; Sequence 29802, Application US/10831901A

; Publication No. US20050100885A1

; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Ecker, David J.

; APPLICANT: Sampath, Rangarajan

; APPLICANT: Freier, Susan M.

; APPLICANT: Massire, Christian

; APPLICANT: Hofstadler, Steven A.

; APPLICANT: Lowery, Kristin Sannes

; APPLICANT: Swayze, Eric

; APPLICANT: Baker, Brenda F.

; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)

; FILE REFERENCE: IS1S0083-100 (BIO100080S)

; CURRENT APPLICATION NUMBER: US/10/831,901A

; CURRENT FILING DATE: 2004-04-26

; PRIOR APPLICATION NUMBER: 60/446,426

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: 60/446,562

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/446,770

; PRIOR FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: 60/446,827

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/446,827

; PRIOR FILING DATE: 2003-06-10

; PRIOR APPLICATION NUMBER: 60/448,579

; PRIOR FILING DATE: 2003-06-27

; SOFTWARE: FastSEQ For Windows Version 4.0

; SEQ ID NO: 29803

; LENGTH: 29573

; TYPE: DNA

; ORGANISM: SARS Coronavirus

US-10-831-901A-29803

Query Match 90.9%; Score 20; DB 21; Length 29573;
Best Local Similarity 75.0%; Pred. No. 0.0089; 0; Gaps 0;
Matches 15; Conservative 5; Mismatches 0; Indels 0;

Qy 1 GUGAACUCACUCCUGAGGCU 20
Db 707 GTGAACTCTCTGGAGTC 726

RESULT 26

US-10-831-901A-29807

; Sequence 29807, Application US/10831901A

; Publication No. US20050100885A1

; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Ecker, David J.

; APPLICANT: Sampath, Rangarajan

; APPLICANT: Freier, Susan M.

; APPLICANT: Massire, Christian

; APPLICANT: Hofstadler, Steven A.

; APPLICANT: Lowery, Kristin Sannes

; APPLICANT: Swayze, Eric

; APPLICANT: Baker, Brenda F.

; APPLICANT: Bennett, C. Frank

; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe

; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)

; FILE REFERENCE: IS1S0083-100 (BIO100080S)

; CURRENT APPLICATION NUMBER: US/10/831,901A

; CURRENT FILING DATE: 2004-04-26

; PRIOR APPLICATION NUMBER: 60/446,426

; PRIOR FILING DATE: 2003-04-28

; PRIOR APPLICATION NUMBER: 60/446,562

; PRIOR FILING DATE: 2003-05-06

; PRIOR APPLICATION NUMBER: 60/446,770

; PRIOR FILING DATE: 2003-04-30

; PRIOR APPLICATION NUMBER: 60/446,827

; PRIOR FILING DATE: 2003-06-10

; PRIOR APPLICATION NUMBER: 60/448,579

; PRIOR FILING DATE: 2003-06-27

; NUMBER OF SEQ ID NOS: 30063

; SOFTWARE: FastSEQ For Windows Version 4.0

; SEQ ID NO: 29807

; LENGTH: 29573

; TYPE: DNA

; ORGANISM: SARS Coronavirus

US-10-831-901A-29802

Query Match 90.9%; Score 20; DB 21; Length 29573;
Best Local Similarity 75.0%; Pred. No. 0.0089; 0; Gaps 0;
Matches 15; Conservative 5; Mismatches 0; Indels 0;

Qy 1 GUGAACUCACUCCUGAGGCU 20
Db 707 GTGAACTCTCTGGAGTC 726

RESULT 25

US-10-831-901A-29803

; Sequence 29803, Application US/10831901A

; Publication No. US20050100885A1

; GENERAL INFORMATION:

; APPLICANT: Crooke, Stanley T.

; APPLICANT: Ecker, David J.

; APPLICANT: Sampath, Rangarajan

; APPLICANT: Freier, Susan M.

; APPLICANT: Massire, Christian

; APPLICANT: Hofstadler, Steven A.

; APPLICANT: Lowery, Kristin Sannes

; APPLICANT: Swayze, Eric

RESULT 27
 US-10-831-901A-29820
 Query Match 90.9%; Score 20; DB 21; Length 29573;
 Best Local Similarity 75.0%; Pred. No. 0.0089; Indels 0; Gaps 0;
 Matches 15; Conservative 5; Mismatches 0;
 CURRENT FILING DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-28
 SEQ ID NO 707 GTGAACTACTCGTGAAGTC 726

RESULT 28
 US-10-831-901A-29820
 Sequence 29820, Application US/10831901A
 GENERAL INFORMATION:
 APPLICANT: Crooke, Stanley T.
 APPLICANT: Ecker, David J.
 APPLICANT: Sampath, Rangarajan
 APPLICANT: Freter, Susan M.
 APPLICANT: Massire, Christian
 APPLICANT: Hofstadler, Steven A.
 APPLICANT: Lowery, Kristin Sannes
 APPLICANT: Swazy, Eric
 APPLICANT: Baker, Brenda F.
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
 Acute Respiratory Syndrome (SARS)
 FILE REFERENCE: ISIS0083-100 (BIO0008US)
 CURRENT APPLICATION NUMBER: US/10/831,901A
 CURRENT FILING DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-30
 PRIOR APPLICATION NUMBER: 60/468,627
 PRIOR FILING DATE: 2003-05-06
 SEQ ID NO 29758
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 29705
 TYPE: DNA
 ORGANISM: SARS Coronavirus
 US-10-831-901A-29758

RESULT 29
 US-10-831-901A-29791
 Sequence 29791, Application US/10831901A
 Publication No. US20050100885A1
 GENERAL INFORMATION:
 APPLICANT: Crooke, Stanley T.
 APPLICANT: Ecker, David J.
 APPLICANT: Sampath, Rangarajan
 APPLICANT: Freter, Susan M.
 APPLICANT: Massire, Christian
 APPLICANT: Hofstadler, Steven A.
 APPLICANT: Lowery, Kristin Sannes
 APPLICANT: Swazy, Eric
 APPLICANT: Baker, Brenda F.
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
 Acute Respiratory Syndrome (SARS)
 FILE REFERENCE: ISIS0083-100 (BIO0008US)
 CURRENT APPLICATION NUMBER: US/10/831,901A
 CURRENT FILING DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: 60/468,562
 PRIOR FILING DATE: 2003-05-06
 SEQ ID NO 29758
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 29705
 TYPE: DNA
 ORGANISM: SARS Coronavirus
 US-10-831-901A-29791

RESULT 28
 US-10-831-901A-29758
 Sequence 29758, Application US/10831901A
 Publication No. US20050100885A1
 GENERAL INFORMATION:
 APPLICANT: Crooke, Stanley T.
 APPLICANT: Ecker, David J.
 APPLICANT: Sampath, Rangarajan
 APPLICANT: Freter, Susan M.
 APPLICANT: Massire, Christian
 APPLICANT: Hofstadler, Steven A.
 APPLICANT: Lowery, Kristin Sannes
 APPLICANT: Swazy, Eric
 APPLICANT: Baker, Brenda F.
 TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
 Acute Respiratory Syndrome (SARS)
 FILE REFERENCE: ISIS0083-100 (BIO0008US)
 CURRENT APPLICATION NUMBER: US/10/831,901A
 CURRENT FILING DATE: 2004-04-26
 PRIOR APPLICATION NUMBER: 60/466,426
 PRIOR FILING DATE: 2003-04-28
 PRIOR APPLICATION NUMBER: 60/468,562
 PRIOR FILING DATE: 2003-05-06
 SEQ ID NO 29791
 SOFTWARE: FastSEQ for Windows Version 4.0
 LENGTH: 29705

```

; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-831-901A-29791

Query Match 90.9%; Score 20; DB 21; Length 29705;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GUGAACUCACUCGGAGCTC 20
Db 760 GTGAACTCTCGTGAAGCTC 779

RESULT 30
US-10-831-901A-29756
Sequence 29756, Application US/10831901A
Publication No. US20050100885A1

GENERAL INFORMATION:
; APPLICANT: Crooke, Stanley T.
; APPLICANT: Becker, David J.
; APPLICANT: Sampath, Rangarajan
; APPLICANT: Freier, Susan M.
; APPLICANT: Massire, Christian
; APPLICANT: Hofstadel, Steven A.
; APPLICANT: Lowery, Kristin Sannes
; APPLICANT: Swayze, Eric
; APPLICANT: Baker, Brenda F.
; APPLICANT: Bennett, C. Frank
; APPLICANT: Bennett, C. Frank
; TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
; TITLE OF INVENTION: Acute Respiratory Syndrome (SARS)
; FILE REFERENCE: 1ST0083-100 (B10Q00080S)
; CURRENT APPLICATION NUMBER: US/10/831,901A
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: 60/466,426
; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ For Windows Version 4.0
; SEQ ID NO: 29756
; LENGTH: 29706
; TYPE: DNA
; ORGANISM: SARS Coronavirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2068
; OTHER INFORMATION: n = A,T,C or G
US-10-831-901A-29756

Query Match 90.9%; Score 20; DB 21; Length 29706;
Best Local Similarity 75.0%; Pred. No. 0.0089;
Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GUGAACUCACUCGGAGCTC 20
Db 760 GTGAACTCTCGTGAAGCTC 779

Search completed: July 21, 2005, 01:08:21
Job time : 609 secs

```

GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw mode1

Run on: July 20, 2005, 18:32:31 ; Search time 1685 Seconds

(without alignment)

632.650 Million cell updates/sec

Title: US-10-848-737-1

Perfect score: 22

Sequence: 1 gugaaucacucugaggcuctt 22

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Listing first 300 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_Dat:*

7: gb_ph:*

8: gb_dl:*

9: gb_dr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	90.9	1706	14	AY322205	AY322205	SARS coro
2	20	90.9	14011	14	AY534758	AY534758	SARS coro
3	20	90.9	26333	14	AY286320	AY286320	SARS coro
4	20	90.9	29013	14	AY461060	AY461060	SARS coro
5	20	90.9	29350	14	AY394999	AY394999	SARS coro
6	20	90.9	29350	14	AY395000	AY395000	SARS coro
7	20	90.9	29350	14	AY395001	AY395001	SARS coro
8	20	90.9	29350	14	AY395002	AY395002	SARS coro
9	20	90.9	29433	14	AY394977	AY394977	SARS coro
10	20	90.9	29530	14	AY394985	AY394985	SARS coro
11	20	90.9	29573	14	AY338174	AY338174	SARS coro
12	20	90.9	29573	14	AY338175	AY338175	SARS coro
13	20	90.9	29573	14	AY348314	AY348314	SARS coro
14	20	90.9	29577	14	AY558094	AY558094	SARS coro
15	20	90.9	29592	14	AY463059	AY463059	SARS coro
16	20	90.9	29620	14	AY395004	AY395004	SARS coro
17	20	90.9	29640	14	AY394978	AY394978	SARS coro
18	20	90.9	29645	14	AY394979	AY394979	SARS coro
19	20	90.9	29646	14	AY394982	AY394982	SARS coro

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	90.9	1706	14	AY322205	AY322205	SARS coro
2	20	90.9	14011	14	AY534758	AY534758	SARS coro
3	20	90.9	26333	14	AY286320	AY286320	SARS coro
4	20	90.9	29013	14	AY461060	AY461060	SARS coro
5	20	90.9	29350	14	AY394999	AY394999	SARS coro
6	20	90.9	29350	14	AY395000	AY395000	SARS coro
7	20	90.9	29350	14	AY395001	AY395001	SARS coro
8	20	90.9	29350	14	AY395002	AY395002	SARS coro
9	20	90.9	29433	14	AY394977	AY394977	SARS coro
10	20	90.9	29530	14	AY394985	AY394985	SARS coro
11	20	90.9	29573	14	AY338174	AY338174	SARS coro
12	20	90.9	29573	14	AY338175	AY338175	SARS coro
13	20	90.9	29573	14	AY348314	AY348314	SARS coro
14	20	90.9	29577	14	AY558094	AY558094	SARS coro
15	20	90.9	29592	14	AY463059	AY463059	SARS coro
16	20	90.9	29620	14	AY395004	AY395004	SARS coro
17	20	90.9	29640	14	AY394978	AY394978	SARS coro
18	20	90.9	29645	14	AY394979	AY394979	SARS coro
19	20	90.9	29646	14	AY394982	AY394982	SARS coro

Prod. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

93	20	90.9	29738	14	AY350750	SARS	coro	c	166	15	68.2	12050	10	MNGU575748	
94	20	90.9	29740	14	AY350755	SARS	coro	c	167	15	68.2	43599	9	HSU15177	
95	20	90.9	29740	14	AY278490	SARS	coro	c	168	15	68.2	50389	1	AE014137	
96	20	90.9	29740	14	AY1310120	SARS	coro	c	169	15	68.2	51430	2	AC014137	
97	20	90.9	29740	14	AY485278	SARS	coro	c	170	15	68.2	54668	6	AX602203	
98	20	90.9	29741	14	AY104486	SARS	coro	c	171	15	68.2	61524	9	AL353725	
99	20	90.9	29741	14	AY485277	SARS	coro	c	172	15	68.2	81786	9	AC00302	
100	20	90.9	29742	14	AY278491	SARS	coro	c	173	15	68.2	83369	8	AL17386	
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111	20	90.9	29765	14	AY194995	SARS	coro	c	184	15	68.2	158692	2	AL76843	
112	20	90.9	29767	14	AY59083	SARS	coro	c	185	15	68.2	147494	1	Streptoco	
113	17	77.3	147433	2	AC137257	Rattus	no	c	180	15	68.2	149515	2	Danio rerio	
c	114	17	77.3	156564	2	AC120103	Rattus	no	c	181	15	68.2	155515	9	AC016909
c	115	16	72.7	221722	2	AC130567	Rattus	no	c	182	15	68.2	157165	2	Bos taurus
c	116	16	72.7	838	8	AK002203	Orzya sativa	coro	c	183	15	68.2	157662	9	Human DNA
c	117	16	72.7	947	8	AK099574	Orzya sativa	coro	c	190	15	68.2	160951	2	CR356245
c	118	16	72.7	120551	9	AY23977	SARS	coro	c	191	15	68.2	160951	9	Homo sapiens
c	119	16	72.7	127267	14	AY13906	SARS	coro	c	192	15	68.2	162105	5	BX001032
c	120	16	72.7	158563	2	AC130567	Rattus	no	c	187	15	68.2	163242	2	Zebrafish
c	121	16	72.7	176629	2	AC130567	Rattus	no	c	188	15	68.2	163263	2	AC121352
c	122	16	72.7	218200	2	AC141165	Rattus	no	c	189	15	68.2	164000	9	Rattus no
c	123	16	72.7	227026	2	AC136659	Rattus	no	c	190	15	68.2	164766	10	AC144792
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c	126	16	72.7	247394	2	AC131227	Rattus	no	c	193	15	68.2	188901	2	AC132886
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c	128	15	68.2	534	6	AK099574	Orzya sativa	coro	c	195	15	68.2	189757	3	Drosophila rerio
c	129	15	68.2	537	6	AK607323	Rattus	no	c	196	15	68.2	190708	9	AC005261
c	130	15	68.2	627	6	AK593704	Rattus	no	c	203	15	68.2	191828	10	Homo sapiens
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ALIGNMENTS									
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LOCUS	AY322205S1	SARS coronavirus Shanhgai LY							
DEFINITION	SARS coronavirus, partial polyprotein genes, partial cds.								
ACCESSION	AY322205								
RESULT 1	AY322205S1	1706 bp	RNA	linear	VRL 21-JUL-2003				
LOCUS	AY322205S1	SARS coronavirus Shanhgai LY							
DEFINITION	SARS coronavirus, partial polyprotein genes, partial cds.								
ACCESSION	AY322205								
VERSION	AY322205.1	GI:32454339							
KEYWORDS			1 of 4						
SEGMENT			SARS coronavirus	Shanhgai LY					
SOURCE			SARS coronavirus	Shanhgai LY					
ORGANISM			Virus	Positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae;					
REFERENCE			1 (bases 1 to 1706)						
AUTHORS			Yuan,Z., Zhang,X., Hu,Y., Lan,S., Wang,H., Zhou,Z. and Wen,Y.						
TITLE			Direct Submission						
JOURNAL			Submitted (12-JUN-2003) Molecular Virology, Shanghai Medical College of Fudan University, 138 Yi Xue Yuan Road, Shanghai 200032, P.R. China						
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RESULT 2	AY534758S1	14011 bp	RNA	linear	VRL 17-MAR-2004				
DEFINITION	SARS coronavirus Sin0409, partial sequence.								
ACCESSION	AY534758								
KEYWORDS			1 of 4						
SEGMENT			SARS coronavirus	Sin0409					
SOURCE			SARS coronavirus	Sin0409					
ORGANISM			Virus	Nidovirales; Coronaviridae; Coronaviridae; Coronaviridae;					
REFERENCE			1 (bases 1 to 14011)						
AUTHORS			Lim,P.L., Kurup,A., Gopalakrishna,G., Chan,K.P., Wong,C.W.,						

Ng, L.C., Se-Thoe, S.Y., Oon, I., Bai, X., Stanton, I.W., Ruan, Y., Miller, I.D., Vega, V.B., James, L., Ooi, P.L., Kai, C.S., Olsen, S.J., Ang, B., and Leo, Y.S.	Miller, I.D., Vega, V.B., James, L., Ooi, P.L., Kai, C.S., Olsen, S.J., Ang, B., and Leo, Y.S.	Severe acute respiratory syndrome (SARS) -	JOURNAL Unpublished Singapore 2003 (bases 1 to 14011)	6 (bases 1 to 26333)
WEI, C.L., Lee, C., Lin, S., Thoreau, H., Vega, V.B., Stanton, L.W. and Ruan, Y.	WEI, C.L., Lee, C., Lin, S., Thoreau, H., Vega, V.B., Stanton, L.W. and Ruan, Y.	Genome Institute of Singapore, 60, Biopolis Street, 02-01, Genome, Singapore 138672, Singapore	JOURNAL Submitted (28-JAN-2004)	REMARK COMMENT On Dec 17, 2003 this sequence version replaced gi: 38304880.
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VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQVQVQVQ VVKHKGQKQVQ SAPPAYKQLOGTFCANEVIGNYOCGHYHTITAKETLYRIGAHUTKMSKXGPVTD VYHTLDESFJGRYMSALNHTPKWKKPQVQVQVQVQVQVQVQVQVQVQVQVQ QRTLGEVFLRKGDKVPLTSLPFLPFLPFLPFLPFLPFLPFLPFLPFL NTNLITQLVDM3MTYQGQFGPTYDQDADVTKIKPHNHEGKTFVFLPSDDTFLRSEAF APALQDQYTRAKAGDNECALLAYSNTKQVQVQVQVQVQVQVQVQVQ

TITLE	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
JOURNAL	Unpublished	REFERENCE 1 (bases 1 to 29350)
REFERENCE	2 (bases 1 to 29350)	AUTHORS The SARS epidemiology consortium of Guangdong
AUTHORS	CONSRM The SARS epidemiology consortium of Guangdong	CONSRM The SARS epidemiology consortium of Guangdong
CONSRM	Direct Submission	From independent foci of epidemic outbreak to large genomic
TITLE	Submitted (19-SEP-2003) Guangdong, China	alteration in late phase viruses: evolution of the SARS-coronavirus
JOURNAL	Location/Qualifiers	Unpublished
FEATURES	1..29350	2 (bases 1 to 29530)
source	/organism="SARS coronavirus ICS5" /mol type="genomic RNA" /isolate="IUC5" /db_xref="taxon:249087"	REFERENCE 2 (bases 1 to 29530)
ORIGIN		AUTHORS The SARS epidemiology consortium of Guangdong
		CONSRM The SARS epidemiology consortium of Guangdong
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		Location/Qualifiers
		1..29530
		/organism="SARS coronavirus HSZ-Bb"
		/mol type="genomic RNA"
		/isolate="HSZ-Bb"
		/db_xref="taxon:249070"
ORIGIN		FEATURES
		source
		/organism="SARS coronavirus HSZ-Bb"
		/mol type="genomic RNA"
		/isolate="HSZ-Bb"
		/db_xref="taxon:249070"
Qy	Query Match 90.9%; Score 20; DB 14; Length 29350; Best Local Similarity 75.0%; Prod. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;	ORIGIN
Db	761 GUGAACUCACUCCUGAGCUC 20 761 GUGAACUCACUCCUGAGCUC 780	ORIGIN
RESULT 9		ORIGIN
LOCUS	AY394977	AY394977
DEFINITION	SARS coronavirus GZ-A, Partial genome.	AY394977
ACCESSION	AY394977	AY394977
VERSION	AY394977.1	AY394977.1
KEYWORDS		GI:37624320
SOURCE		RESULT 11
ORGANISM	SARS coronavirus GZ-A	LOCUS AY38174
	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;	DEFINITION SARS coronavirus Taiwan TC1, complete genome.
	Coronaviridae; Coronavirus.	ACCESSION AY38174
REFERENCE	1 (bases 1 to 29433)	VERSION AY38174..1 GI:32493129
AUTHORS	CONSRM The SARS epidemiology consortium of Guangdong	KEYWORDS
CONSRM	From independent foci of epidemic outbreak to large genomic	SARS coronavirus Taiwan TC1
TITLE	alteration in late phase viruses: evolution of the SARS-coronavirus	SARS coronavirus Taiwan TC1
JOURNAL	Unpublished	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
FEATURES	2 (bases 1 to 29433)	REFERENCE 1 (bases 1 to 29530)
source	/organism="SARS coronavirus GZ-A" /mol type="genomic RNA" /isolate="GZ-A" /db_xref="taxon:249062"	AUTHORS Chang,J.-G.C., Lin,T.-H., Chen,C.-M., Lin,C.-S., Chan,W.-L. and Shih,M.-C.
ORIGIN		TITLE JOURNAL
		Unpublished 2 (bases 1 to 29573)
		AUTHORS Chang,J.-G.C., Lin,T.-H., Chen,C.-M., Lin,C.-S., Chan,W.-L. and Shih,M.-C.
		TITLE JOURNAL
		Direct Submission Submitted (08-JUL-2003) Department of Molecular Medicine, China Medical University Hospital, 2, Yuh Der Road, Taichung, Taiwan 404, Taiwan
		REMARK Amino acid sequence updated by submitter
		FEATURES Location/Qualifiers
		source
		1..29573
		/organism="SARS coronavirus Taiwan TC1" /mol type="genomic RNA"
		/isolate="TC1"
		/db_xref="taxon:237639"
		/noFE="clinical specimen"
		join(196..13329,13329..21416)
RESULT 10		CDS
AY394985	AY394985	DEFINITION SARS coronavirus HSZ-Bb, complete genome.
LOCUS	AY394985	ACCESSION AY394985
DEFINITION	SARS coronavirus HSZ-Bb, complete genome.	VERSION AY394985..1 GI:37624328
ACCESSION	AY394985	SOURCE SARS coronavirus HSZ-Bb
VERSION		ORGANISM SARS coronavirus HSZ-Bb

CDS

RESULT	1.2	Y338175	AY338175	29573	bp	RNA	linear	VRL 28-JUL-2003
OCUS	Coronavirus	Taiwan	TC2, complete genome.					
DEFINITION	SARS coronavirus	Taiwan	TC2,					
CCSSION	AY338175	AY338175						
ERSION	AV338175.1	GI:32493130						
EWORDS								
OURCE	SARS coronavirus	Taiwan	TC2					
ORGANISM	SARS coronavirus	Taiwan	TC2					
	Virus	positive-strand viruses, no DNA stage; Nidovirales;						
	Coronaviridae: Coronavirus.							
EFERENCE	1. (bases 1 to 29573)							
AUTHORS	Chang, J., Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.							
TITLE								
JOURNAL	SARS coronavirus TC2, clinical specimen							
EFERENCE	Unpublished							
AUTHORS	2. (bases 1 to 29573)							
TITLE	Chang, J., Lin, T., Chen, C., Lin, T., Chan, W. and Shih, M.							
JOURNAL	Direct Submission							
	Submitted (09-JUL-2003) Department of Molecular Medicine, China							
	Medical University Hospital, 2, Yuh Der Road, Taichung, Taichung							

REFERENCE 3 (bases 1 to 29573)
 AUTHORS Chang,J., Lin,T., Chen,C., Lin,T., Chan,W. and Shih,M.
 TITLE Direct Submission
 JOURNAL Submitted (28-JUN-2003) Department of Molecular Medicine, China
 MEDICAL UNIVERSITY Hospital, 2, Yuh Der Road, Taichung, Taichung
 404, Taiwan
 REMARK Amino acid sequence updated by submitter

source: SARS coronavirus Taiwan TC2
 /organism="SARS coronavirus Taiwan TC2"
 /mol_type="genomic RNA"
 /isolate="TC2"
 /db_xref="237640"
 /note="Clinical specimen"
 join(19, 13329, 13328, 21416)
 /product="nonstructural polyprotein pp1ab"
 /protein_id="AAQ01606_1"
 /codon_start=1
 /db_xref="GI:33285979"
 /transl_start="MESLIVLGNEKTHVQLSLPVQDVLVPGFDSVREALLSPARE
 HLKNGTCGLVLEKGVDLQLEQPVFIRKSDALSTNHGKVVELAEMDGIOYGRSGI
 WTYKGVPGVPEIAYNVLLRKNGKAGGHSYGLDCKDSTKDLARAGSMCLTSRQ
 LDYIESKGKGVCCRDBHEBIAHNTFSDKSYEHTOPPEIKSAKKDFTFKGBCPKFVFP
 LNSKVKVQIOPREUKKTEGFMGRISYSSVPAOCBNMILSTLJKCNEHDAEVSNQTC
 DFLKATCCHCCCTTVEGPMTCGKPTVPAVQKPTVPAVQKPTVPAVQKPTVPAVQK
 IETLKRKGTRCTFGGCVFAYVGCKYCNKRAYNVPRAASIDGSGHHTGIGDNVTELNB
 DLTSRREVNINTVGDPHLNEVATIILASASASATSDFTLKSPLKSPKTVIPEOOG
 VTCMCGKPTVPAVQKPTVPAVQKPTVPAVQKPTVPAVQKPTVPAVQKPTVPAVQK

ORIGIN	Query Match 90.9%; Score 20; DB 14; Length 29620; Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;	Source 1. .29645 /organism="SARS coronavirus GZ-C" /mol_type="genomic RNA" /isolate="GZ-C" /db_xref="taxon:249064"
Qy	1 GUGAACUCACUCGUGAGCUC 20 [: : : : : : Db 729 GTGAACTACTCGTCGTC 748	ORIGIN Query Match 90.9%; Score 20; DB 14; Length 29645; Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
RESULT 17		RESULT 19
LOCUS	AY394978 29640 bp RNA	LOCUS AY394982 29646 bp RNA
DEFINITION	SARS coronavirus GZ-B, complete genome.	DEFINITION SARS coronavirus HGZ8L1-B, partial genome.
ACCESSION	AY394978	ACCESSION AY394982
VERSION	AY394978.1	VERSION AY394982.1
KEYWORDS		KEYWORDS SARS coronavirus HGZ8L1-B
SOURCE	SARS coronavirus GZ-B	SOURCE SARS coronavirus HGZ8L1-B
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
REFERENCE	1 (bases 1 to 29640)	REFERENCE 1 (bases 1 to 29646)
AUTHORS		AUTHORS
CONSRM	The SARS epidemiology consortium of Guangdong	CONSRM The SARS epidemiology consortium of Guangdong
TITLE	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus	TITLE From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus
JOURNAL	Unpublished	JOURNAL Unpublished
REFERENCE	2 (bases 1 to 29640)	REFERENCE 2 (bases 1 to 29646)
AUTHORS		AUTHORS
CONSRM	The SARS epidemiology consortium of Guangdong	CONSRM The SARS epidemiology consortium of Guangdong
TITLE	Direct Submission	TITLE Direct Submission
JOURNAL	Submitted (19-SEP-2003) Guangdong, China	JOURNAL Submitted (19-SEP-2003) Guangdong, China
FEATURES		FEATURES Location/Qualifiers
REFERENCE	1. .29640	REFERENCE 1. .29646
AUTHORS	/organism="SARS coronavirus GZ-B"	AUTHORS /organism="SARS coronavirus HGZ8L1-B"
CONSRM	/mol_type="genomic RNA"	CONSRM /mol_type="genomic RNA"
TITLE	/isolate="GZ-B"	TITLE /isolate="HGZ8L1-B"
JOURNAL	/db_xref="taxon:249063"	JOURNAL /db_xref="taxon:249067"
ORIGIN		ORIGIN
Qy	Query Match 90.9%; Score 20; DB 14; Length 29640; Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;	Query Match 90.9%; Score 20; DB 14; Length 29646; Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
RESULT 18		RESULT 20
LOCUS	AY394979 29645 bp RNA	LOCUS AY395003 29647 bp RNA
DEFINITION	SARS coronavirus GZ-C, complete genome.	DEFINITION SARS coronavirus ZS-C, complete genome.
ACCESSION	AY394979	ACCESSION AY395003
VERSION	AY394979.1	VERSION AY395003.1
KEYWORDS		KEYWORDS SARS coronavirus ZS-C
SOURCE	SARS coronavirus GZ-C	SOURCE SARS coronavirus ZS-C
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
REFERENCE	1 (bases 1 to 29645)	REFERENCE 1 (bases 1 to 29647)
AUTHORS		AUTHORS
CONSRM	The SARS epidemiology consortium of Guangdong	CONSRM The SARS epidemiology consortium of Guangdong
TITLE	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus	TITLE From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus
JOURNAL	Unpublished	JOURNAL Unpublished
FEATURES	2 (bases 1 to 29645)	REFERENCE 2 (bases 1 to 29647)

AUTHORS	The SARS epidemiology consortium of Guangdong									
CONSRIM	The SARS epidemiology consortium of Guangdong									
JOURNAL	Direct Submission (19-SEP-2003) Guangdong, China									
FEATURES	1. 29647 /organism="SARS coronavirus ZS-C" /mol type="genomic RNA" /isolate="ZS-C" /db_xref="taxon:249088"									
source										
ORIGIN										
RESULT 21	Query Match 90.9%; Score 20; DB 14; Length 29647;									
AV559086	Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;									
LOCUS	SARS coronavirus Sin849, complete genome.									
DEFINITION	AY559086									
ACCESSION	AY559086.1									
VERSION	GI:45645003									
KEYWORDS	SARS coronavirus Sin849									
SOURCE	SARS coronavirus Sin849									
ORGANISM	SARS coronavirus; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.									
REFERENCE	1. (bases 1 to 29661)									
AUTHORS	Vega, V.B., Ruan, Y., Liu, J., Lee, W.H., Wei, C.L., Se-Thoe, S.Y., Tang, K.F., Zhang, T., Long, P.M. and Liu, E.T.									
TITLE	Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003									
JOURNAL	(er) BMC Infect. Dis. 4 (1), 32 (2004)									
PUBLMED	15347429									
REFERENCE	2. (bases 1 to 29661)									
AUTHORS	Vega, V.B., Ruan, Y., Liu, J., Lee, W.H., Wei, C.L., Se Thoe, S.Y., Tang, K.F., Zhang, T., Lin, S., Kolatkar, P., Ooi, E.E., Ee, L.A., Stanton, L.W., Long, P.M. and Liu, E.T.									
TITLE	Direct Submission									
JOURNAL	Submitted (24-FEB-2004) Genome Institute of Singapore, 60, Biopolis Street #02-01, Genome, Singapore 1386782, Singapore									
FEATURES	1. 29661 /organism="SARS coronavirus Sin849" /mol type="genomic RNA" /db_xref="taxon:267398" /country="Singapore"									
source										
ORIGIN										
RESULT 22	Query Match 90.9%; Score 20; DB 14; Length 29661;									
AV394988	Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;									
LOCUS	AY394988									
DEFINITION	SARS coronavirus JMD, partial genome.									
ACCESSION	AY394988.1									
VERSION	GI:37624331									
SOURCE	SARS coronavirus JMD									
ORGANISM	SARS coronavirus									
REFERENCE	1. 29665									
AUTHORS	The SARS epidemiology consortium of Guangdong									
CONSRIM	The SARS epidemiology consortium of Guangdong									
JOURNAL	From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus									
FEATURES	Unpublished									
source	2 (bases 1 to 29665)									
ORIGIN										
RESULT 23	Query Match 90.9%; Score 20; DB 14; Length 29665;									
AY559082	Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;									
LOCUS	AY559082									
DEFINITION	SARS coronavirus Sin852, complete genome.									
ACCESSION	AY559082.1									
VERSION	GI:45644996									
KEYWORDS										
SOURCE	SARS coronavirus Sin852									
ORGANISM	SARS coronavirus Sin852									
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.									
AUTHORS	1 (bases 1 to 29670)									
VEGA	Vega, V.B., Ruan, Y., Liu, J., Lee, W.H., Wei, C.L., Se-Thoe, S.Y., Tang, K.F., Zhang, T., Lin, S., Kolatkar, P.R., Ooi, E.E., Ling, A.E., Stanton, L.W., Long, P.M. and Liu, E.T.									
TITLE	Mutational dynamics of the SARS coronavirus in cell culture and human populations isolated in 2003									
JOURNAL	(er) BMC Infect. Dis. 4 (1), 32 (2004)									
PUBLMED	15347429									
REFERENCE	2 (bases 1 to 29670)									
AUTHORS	Vega, V.B., Ruan, Y., Liu, J., Lee, W.H., Wei, C.L., Se Thoe, S.Y., Tang, K.F., Zhang, T., Lin, S., Kolatkar, P., Ooi, E.E., Ee, L.A., Stanton, L.W., Long, P.M. and Liu, E.T.									
TITLE	Direct Submission									
JOURNAL	Submitted (24-FEB-2004) Genome Institute of Singapore, 60, Biopolis Street #02-01, Genome, Singapore 1386782, Singapore									
FEATURES	1. 29661 /organism="SARS coronavirus Sin849" /mol type="genomic RNA" /db_xref="taxon:267398" /country="Singapore"									
source										
ORIGIN										
RESULT 24	Query Match 90.9%; Score 20; DB 14; Length 29670;									
AY394988	Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;									
LOCUS	AY394988									
DEFINITION	SARS coronavirus JMD, partial genome.									
ACCESSION	AY394988.1									
VERSION	GI:37624331									
SOURCE	SARS coronavirus JMD									
ORGANISM	SARS coronavirus									
REFERENCE	1. 29665									
AUTHORS	The SARS epidemiology consortium of Guangdong									
CONSRIM	The SARS epidemiology consortium of Guangdong									
JOURNAL	Submitted (19-SEP-2003) Guangdong, China									
FEATURES	Location/Qualifiers									
source	1. 29665									
ORIGIN										
RESULT 25	Query Match 90.9%; Score 20; DB 14; Length 29670;									
AY394988	Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;									
LOCUS	AY394988									
DEFINITION	SARS coronavirus JMD									
ACCESSION	AY394988.1									
VERSION	GI:37624331									
SOURCE	SARS coronavirus JMD									
ORGANISM	SARS coronavirus									
REFERENCE	1. 29665									
AUTHORS	The SARS epidemiology consortium of Guangdong									
CONSRIM	The SARS epidemiology consortium of Guangdong									
JOURNAL	Submitted (19-SEP-2003) Guangdong, China									
FEATURES	Location/Qualifiers									
source	1. 29665									
ORIGIN										
RESULT 26	Query Match 90.9%; Score 20; DB 14; Length 29670;									
AY394988	Best Local Similarity 75.0%; Pred. No									

FEATURES source Location/Qualifiers 1. .29/05 /organism="SARS coronavirus Sin2677" /virion /mol_type="genomic RNA" /isolate="SIN2677" /db_xref="Saxon:235413" /country="Singapore"

ORIGIN Query Match 90.9%; Score 20; DB 14; Length 29705; Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUGGAGCTC 20
Db 760 GTGAACTCACTCGTGAAGCTC 779

RESULT 28
LOCUS AY394980 29705 bp RNA linear VRL 29-JAN-2004

DEFINITION SARS coronavirus GZ-D, partial genome.

VERSION AY394980.1 GI:37624323

KEYWORDS

ORGANISM SARS coronavirus GZ-D

SARS coronavirus; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronaviruses.

REFERENCE 1 (bases 1 to 29705)

CONTRSM The SARS epidemiology consortium of Guangdong TITLE From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus JOURNAL Unpublished 2 (bases 1 to 29705)

REFERENCE AUTHORS The SARS epidemiology consortium of Guangdong JOURNAL Direct Submission 19-SEP-2003 Guangdong, China

FEATURES source Location/Qualifiers 1. .29/05 /organism="SARS coronavirus GZ-D" /mol_type="genomic RNA" /isolate="GZ-D" /db_xref="taxon:249065"

ORIGIN Query Match 90.9%; Score 20; DB 14; Length 29705; Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUGGAGCTC 20
Db 730 GTGAACTCACTCGTGAAGCTC 749

RESULT 29
LOCUS AY283797 29706 bp RNA linear VRL 12-AUG-2003

DEFINITION SARS coronavirus Sin2748, complete genome.

VERSION AY283797.1 GI:30468045

KEYWORDS

ORGANISM SARS coronavirus Sin2748

SARS coronavirus Sin2748

Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronaviruses.

REFERENCE 1 (bases 1 to 29706)

AUTHORS Ruan,Y., Wei,C.L., Ling,A.E., Vega,V.B., Thoreau,H., Se Thoe,S.Y., Chia,J.-M., Ng,P., Chiu,K.P., Lim,L., Zhang,T., Chan,K.P., Con,L.E.L., Ng,M.L., Leo,S.Y., Ng,L.F.P., Ren,E.C., Stanton,L.W.,

TITLE Long, P.M. and Liu, E.T. Comparative full-length genome sequence analysis of 14 SARS coronavirus isolates and common mutations associated with putative origins of infection

JOURNAL Lancet 361 (9371), 1779-1785 (2003)

MEDLINE 22667074

PUBMED 12781537

REMARK Erratum in: Lancet. 2003 May 24;361(9371):1832.

REFERENCE 2 (bases 1 to 29706)

AUTHORS Wei,C.L., Thoreau,H., Chia,J.-M., Chiu,K.P., Ng,P., Lim,L., Lambert,E., Zhang,T., Wong,M., Se Thoe,S.Y., Chan,K.P. and Ruan,Y.

TITLE Direct Submission (27-APR-2003) Genome Institute of Singapore, 1 Science Park Road, The Capricorn #05-01, Singapore 117528, Singapore

JOURNAL Location/Qualifiers 1. .29/06 /organism="SARS coronavirus Sin2748" /virion /mol_type="genomic RNA" /isolate="SIN2748" /db_xref="taxon:235411"

FEATURES source Location/Qualifiers 1. .29/06 /organism="SARS coronavirus Sin2748" /virion /mol_type="genomic RNA" /isolate="SIN2748" /db_xref="taxon:235411"

ORIGIN Query Match 90.9%; Score 20; DB 14; Length 29706; Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUGGAGCTC 20
Db 760 GTGAACTCACTCGTGAAGCTC 779

RESULT 30
LOCUS AY394987 29709 bp RNA linear VRL 29-JAN-2004

DEFINITION SARS coronavirus HZS2-Fb, complete genome.

ACCESSION AY394987

VERSION AY394987.1 GI:37624330

KEYWORDS

SOURCE SARS coronavirus HZS2-Fb

ORGANISM SARS coronavirus HZS2-Fb Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronaviruses.

REFERENCE 1 (bases 1 to 29709)

AUTHORS CONSRSM The SARS epidemiology consortium of Guangdong TITLE From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus JOURNAL Unpublished 2 (bases 1 to 29709)

REFERENCE AUTHORS CONSRSM The SARS epidemiology consortium of Guangdong TITLE Direct Submission (19-SEP-2003) Guangdong, China JOURNAL Submitted (19-SEP-2003) Guangdong, China

FEATURES source Location/Qualifiers 1. .29/09 /organism="SARS coronavirus HZS2-Fb" /mol_type="genomic RNA" /isolate="HZS2-Fb"

ORIGIN Query Match 90.9%; Score 20; DB 14; Length 29709; Best Local Similarity 75.0%; Pred. No. 0.013; Matches 15; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GUGAACUCACUGGAGCTC 20
Db 734 GTGAACTCACTCGTGAAGCTC 753

Search completed: July 21, 2005, 00:02:38

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